

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 27, 2005, 17:56:17 ; Search time 165 seconds  
(without alignments)  
147.672 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RSRRATEVTPVVPTVTDYD.....AGGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseqp\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	63	5	Abb76407 Osteopont
2	236	70.9	87	5	Aae18619 Biosynthe
3	207	62.2	40	5	Abb76406 Osteopont
4	201	60.4	40	5	Abb76410 Osteopont
5	200	60.1	40	5	Abb76404 Osteopont
6	200	60.1	40	5	Abb76411 Osteopont
7	181	54.4	49	5	Abb76405 Osteopont
8	181	54.4	192	5	Abg79674 Tumour in
9	181	54.4	218	8	Adsi2215 Human the
10	181	54.4	243	8	Adj67551 Human ova
11	181	54.4	243	8	Adj67676 Human ova
12	181	54.4	273	7	Aao30815 Human cel
13	181	54.4	278	7	Adm47287 Osteopont
14	181	54.4	279	8	Adsi10984 Human the
15	181	54.4	282	2	Aar30701 Isoform o
16	181	54.4	286	6	Abp58125 Human ost
17	181	54.4	287	4	Aab30575 A human ova
18	181	54.4	287	5	Abg96388 Human ova
19	181	54.4	287	6	Abra7551 Breast ca
20	181	54.4	287	6	Abra7551 Breast ca
21	181	54.4	287	7	Abp58123 Human cer
22	181	54.4	287	7	Adb75483 Prostata
23	181	54.4	287	8	Adq88475 Human OPN
24	181	54.4	290	7	Adm47215 Osteopoti
25	181	54.4	296	2	Aar30700 Human uro
	181	54.4	299	6	Abp58124 Human ost

ALIGNMENTS

RESULT 1

ID ABB76407 standard; protein; 63 AA.

XX AC

XX ABB76407;

XX 27-AUG-2002 (first entry)

XX Osteopontin-derived peptide.

XX Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;

XX cell differentiation.

XX Homo sapiens.

XX WO200232940-A2.

XX 25-APR-2002.

XX 18-OCT-2001; 2001WO-US032457.

XX 18-OCT-2000; 2000US-0241248P.

XX 05-OCT-2001; 2001US-0327273P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Askar S, Salcedo J;

XX WPI; 2002-479661/51.

XX Osteopontin derived peptides useful in implants e.g. dental screws or fixtures, and orthopedic joints.

XX Claim 1; Page 8; 64pp; English.

XX The present sequence is an osteopontin-derived peptide, which regulates cell development and binds to an integrin on a cell surface. The invention provides an osteopontin containing implant which increases the rate of osseointegration and the percentage of bone apposition. The implant includes osteopontin, an active fragment of osteopontin or an osteopontin-derived peptide such as the present claimed peptide. Claimed osteopontin derived peptides of the invention (see ABB76403-11) bind to various cell types and play important roles in cellular differentiation and/or motility. These cells include osteoprogenitor cells, tumour cells, macrophages, peritoneal cells, endothelial cells, epithelial cells, eosinophils, stem cells, limited potential precursor cells, precursor cells, committed precursor cells, and differentiated cells. The peptides are also active as antiinflammatory agents. Antibodies provide a



CC mechanism to abolish or attenuate the activities of the claimed peptides.  
CC The implant can be used in an osteopontin containing cell recruitment  
CC system, to induce new tissue formation in a subject, and to promote cell  
CC differentiation (all claimed). The implants include surgical implants  
CC such as dental screws or fixtures, jaw modification implants, face  
CC reconstitution implants, orthopaedic implants e.g. orthopaedic screws,  
CC rods or joints such as hip or knee replacement implants  
XX

SQ Sequence 40 AA;

Query Match 62.2%; Score 207; DB 5; Length 40;

Best Local Similarity 100.0%; Pred. No. 5.6e-16; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSRRAVEFTVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40  
|||||  
DB 1 RSRRAVEFTVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40

RESULT 4

ABB76410  
ID ABB76410 standard; protein; 40 AA.

AC ABB76410;

DT 27-AUG-2002 (first entry)

DE Osteopontin-derived peptide.

KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;  
cell differentiation.

OS Homo sapiens.

PN WO200232940-A2.

PD 25-APR-2002.

PF 18-OCT-2001; 2001WO-US032457.

PR 18-OCT-2000; 2000US-0241248P.

PS 05-OCT-2001; 2001US-0327273P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Askar S, Salcedo J;

XX WPI; 2002-479661/51.

XX Osteopontin derived peptides useful in implants e.g. dental screws or  
fixtures, and orthopedic joints.

XX Claim 1; Page 8; 64pp; English.

XX The present sequence is an osteopontin-derived peptide, which regulates  
cell development and binds to an integrin on a cell surface. The  
invention provides an osteopontin containing implant which increases the  
rate of osseointegration and the percentage of bone apposition. The  
implant includes osteopontin, an active fragment of osteopontin or an  
osteopontin-derived peptide such as the present claimed peptide. Claimed  
osteopontin-derived peptides of the invention (see ABB76403-11) bind to  
various cell types and play important roles in cellular differentiation  
and/or motility. These cells include osteoprogenitor cells, tumour cells,  
macrophages, peritoneal cells, endothelial cells, epithelial cells,  
eosinophils, stem cells, limited potential precursor cells, precursor  
cells, committed precursor cells, and differentiated cells. The peptides  
are also active as antiinflammatory agents. Antibodies provide a  
mechanism to abolish or attenuate the activities of the claimed peptides.  
The implant can be used in an osteopontin containing cell recruitment  
system, to induce new tissue formation in a subject, and to promote cell  
differentiation (all claimed). The implants include surgical implants  
such as dental screws or fixtures, jaw modification implants, face  
reconstitution implants, orthopaedic implants e.g. orthopaedic screws,

CC rods or joints such as hip or knee replacement implants

XX Sequence 40 AA;

Query Match 60.4%; Score 201; DB 5; Length 40;

Best Local Similarity 97.5%; Pred. No. 2.6e-15; Mismatches 39; Conservative 0; Indels 0; Gaps 0;

QY 1 RSRRAVEFTVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40  
|||||  
DB 1 RSRRAVEFTVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40

RESULT 5

ABB76404  
ID ABB76404 standard; protein; 40 AA.

AC ABB76404;

DT 27-AUG-2002 (first entry)

DE Osteopontin-derived peptide OC-1016.

KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;  
cell differentiation.

OS Homo sapiens.

PN WO200232940-A2.

PD 25-APR-2002.

PF 18-OCT-2001; 2001WO-US032457.

PR 18-OCT-2000; 2000US-0241248P.

XX 05-OCT-2001; 2001US-0327273P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Askar S, Salcedo J;

XX WPI; 2002-479661/51.

XX Osteopontin derived peptides useful in implants e.g. dental screws or  
fixtures, and orthopedic joints.

XX Claim 1; Page 59; 64pp; English.

XX The present sequence is osteopontin-derived peptide OC-1016, which  
regulates cell development and binds to an integrin on a cell surface.  
The invention provides an osteopontin containing implant which increases  
the rate of osseointegration and the percentage of bone apposition. The  
implant includes osteopontin, an active fragment of osteopontin or an  
osteopontin-derived peptide such as the present, preferred peptide.  
Claimed osteopontin derived peptides of the invention (see ABB76403-11)  
bind to various cell types and play important roles in cellular  
differentiation and/or motility. These cells include osteoprogenitor  
cells, tumour cells, macrophages, peritoneal cells, endothelial cells,  
epithelial cells, eosinophils, stem cells, limited potential precursor  
cells, precursor cells, committed precursor cells, and differentiated  
cells. The peptides are also active as antiinflammatory agents.  
Antibodies provide a mechanism to abolish or attenuate the activities of  
the claimed peptides. The implant can be used in an osteopontin  
containing cell recruitment system, to induce new tissue formation in a  
subject, and to promote cell differentiation (all claimed). The implants  
include surgical implants such as dental screws or fixtures, jaw  
modification implants, face reconstitution implants, orthopaedic implants  
e.g. orthopaedic screws, rods or joints such as hip or knee replacement  
implants

XX Sequence 40 AA;

Query Match 60.1%; Score 200; DB 5; Length 40;

Best Local Similarity	97.5%;	Pred. NO. 3.4e-15;	
Matches	39;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1	RSRRATEVFTVPVPTDYDGRGDSVYGRSKSKFRRP	40
DB	1	RSRRATEVFTVPVPTDYDGRGDSVYGLRSKSKFRRP	40
RESULT 6			
ABB76411			
ID	ABB76411	standard; protein; 40 AA.	
XX	AC	ABB76411;	
XX	XX	27-AUG-2002 (first entry)	
XX	DE	Osteopontin-derived peptide mOC-1016.	
XX	DE	Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;	
KW	KW	cell differentiation.	
XX	XX	Homo sapiens.	
OS	XX		
XX	XX		
FH	Key	Location/Qualifiers	
FT	Modified-site	1	
FT		/note= "N-terminal acetyl"	
XX	XX		
PN	WO200232940-A2.		
XX	XX	25-APR-2002.	
PD	XX		
PF	XX	18-OCT-2001; 2001WO-US032457.	
XX	XX		
PR	XX	18-OCT-2000; 2000US-0241248P.	
PR	XX	05-OCT-2001; 2001US-0327273P.	
XX	XX	(CHIL-) CHILDRENS MEDICAL CENT.	
PA	XX		
XX	XX	Askar S, Salcedo J;	
PI	XX		
XX	XX	WPI; 2002-479661/51.	
DR	XX		
PT	XX	Osteopontin derived peptides useful in implants e.g. dental screws or	
PT	XX	fixtures, and orthopedic joints.	
XX	XX		
PS	XX	Claim 1; Page 59; 64pp; English.	
XX	XX		
CC	CC	The present sequence is osteopontin-derived peptide mOC-1016, which	
CC	CC	regulates cell development and binds to an integrin on a cell surface.	
CC	CC	The invention provides an osteopontin containing implant which increases	
CC	CC	the rate of osseointegration and the percentage of bone apposition. The	
CC	CC	implant includes osteopontin, an active fragment of osteopontin or an	
CC	CC	osteopontin-derived peptide such as the present, preferred peptide.	
CC	CC	Claimed osteopontin derived peptides of the invention (see ABB76403-11)	
CC	CC	bind to various cell types and play important roles in cellular	
CC	CC	differentiation and/or motility. These cells include osteoprogenitor	
CC	CC	cells, tumour cells, macrophages, perosteal cells, endothelial cells,	
CC	CC	epithelial cells, eosinophils, stem cells, limited potential precursor	
CC	CC	cells, precursor cells, committed precursor cells, and differentiated	
CC	CC	cells. The peptides are also active as antiinflammatory agents.	
CC	CC	Antibodies provide a mechanism to abolish or attenuate the activities of	
CC	CC	the claimed peptides. The implant can be used in an osteopontin	
CC	CC	containing cell recruitment system, to induce new tissue formation in a	
CC	CC	subject, and to promote cell differentiation (all claimed). The implants	
CC	CC	include surgical implants such as dental screws or fixtures, jaw	
CC	CC	modification implants, face reconstruction implants, orthopaedic implants	
CC	CC	e.g. orthopaedic screws, rods or joints such as hip or knee replacement	
CC	XX	implants	
XX	XX		
XX	XX	Sequence 40 AA;	
XX	XX		

Query Match

Best Local Similarity 60.1%; Score 200; DB 5; Length 40;

Query 97.5%; Pred. NO. 3.4e-15;

RESULT 8  
 ABG79674  
 ID ABG79674 standard; protein; 192 AA.  
 AC AC  
 XX ABG79674;  
 15-NOV-2002 (first entry)  
 XX  
 DE Tumour involved gene (TIG) splice variant protein, NV-5.  
 XX  
 KW Human; splice variant; tumour-involved gene; TIG;  
 KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;  
 KW endothelial cell; cell differentiation; cell proliferation; apoptosis;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002086384-A1.  
 XX  
 XX 04-JUL-2002.  
 XX  
 XX 13-MAR-2001; 2001US-00805020.  
 XX  
 XX 14-MAR-2000; 2000IL-00135402.  
 XX 16-MAY-2000; 2000IL-00136154.  
 XX  
 XX (LEVI/) LEVINE Z.  
 XX (DAVI/) DAVID A.  
 XX (ROMA/) ROMANO C.  
 XX (BERN/) BERNSTEIN J.  
 XX  
 XX Levine Z, David A, Romano C, Bernstein J;  
 XX  
 XX WPI; 2002-635679/68.  
 XX N-PSDB; ABS65204.  
 XX  
 XX Novel nucleic acid sequence, which is an alternative splicing variant of  
 XX tumor involved genes, useful for detecting cancer, predisposition to  
 XX cancer, for evaluating cancer state and in gene therapy for treating  
 XX cancer.  
 XX  
 XX Claim 4; Page 70-71; 180pp; English.  
 XX  
 XX The invention discloses isolated human nucleic acid alternative splicing  
 XX variants that are all tumour-involved genes (TIGs). The nucleic acid and  
 XX polypeptides are useful for determining the level of a nucleic acid or  
 XX polypeptide in a biological sample, for detecting a variant nucleic acid  
 XX or polypeptide sequence in a biological sample, for determining the level  
 XX of variant nucleic acid or polypeptide sequences in a biological sample  
 XX and for determining the ratio between the level of variant sequence in a  
 XX first biological sample and the level of the original sequence from which  
 XX the variant has been varied by alternative splicing in a second  
 XX biological sample and for raising antibodies. A pharmaceutical  
 XX composition comprising a carrier and the nucleic acid, is useful for  
 XX treating diseases (e.g. cancer) that can be ameliorated or cured by  
 XX increasing or decreasing the level of the encoded protein. The nucleic  
 XX acids are also useful for diagnostic purposes, especially for detecting  
 XX cancer or a predisposition to cancer, for evaluating the state or  
 XX aggressiveness of cancer disease, in basic research, for understanding  
 XX the physiological function of the original TIG, in targeting or  
 XX developing pharmaceuticals, for distinguishing various stages in the life  
 XX cycle of the same type of cells which may be helpful for the development  
 XX of pharmaceuticals for various cancer stages in which cell cycle is non-  
 XX normal, for determining mutations in tumour-involved genes and in gene  
 XX therapy. The polypeptides are useful for identifying compounds capable of  
 XX binding to the variant product and modulating its activity and for  
 XX modulating endothelial differentiation and proliferation, as well as to  
 XX modulate apoptosis either ex vivo or in vivo. The sequences presented in  
 XX ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs  
 XX disclosed  
 XX  
 XX Sequence 192 AA;

Query Match 54.4%; Score 181; DB 5; Length 192;  
 Best Local Similarity 97.2%; Pred. No. 2.5e-12;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 ATEVTPVVPVTDYDGRGDSVVYGRRSKSKKFRFP 40  
 DB 142 ATEVTPVVPVTDYDGRGDSVVYGLRSKSKKFRFP 177  
 RESULT 9  
 ADS12215  
 ID ADS12215 standard; protein; 218 AA.  
 XX  
 AC ADS12215;  
 XX  
 XX 16-DEC-2004 (first entry)  
 XX  
 XX Human therapeutic contig protein - SEQ ID 2452.  
 XX  
 XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
 KW aplastic anaemia; cancer; wound healing; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..218 /label= Unknown, OTHER  
 FT /note= "OTHER = In-frame STOP codon"  
 XX  
 XX WO2004080148-A2.  
 XX  
 XX 23-SEP-2004.  
 XX  
 XX 30-SEP-2003; 2003WO-US030720.  
 XX  
 XX 02-OCT-2002; 2002US-0416186P.  
 XX (NUVE-) NUVELO INC.  
 XX  
 XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
 XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
 XX WPI: 2004-668857/65.  
 XX N-PSDB; ADS11617.  
 XX  
 XX New polynucleotide, useful in preparing a composition for diagnosing or  
 XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
 XX aplastic anemia or cancer for promoting wound healing.  
 XX  
 XX Example 2; SEQ ID NO 2452; 718pp; English.  
 XX  
 XX The invention relates to a novel isolated polynucleotide and the encoded  
 XX polypeptide. The molecules of the invention demonstrate antiinflammatory,  
 XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
 XX be useful in preparing a composition for diagnosing or treating  
 XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
 XX disorders, such as aplastic anaemia or cancer, as well as for promoting  
 XX wound healing. The molecules may also be utilised during gene therapy  
 XX procedures. The current sequence is that of a human therapeutic contig  
 XX protein of the invention.  
 XX  
 XX Sequence 218 AA;  
 QY 5 ATEVTPVVPVTDYDGRGDSVVYGRRSKSKKFRFP 40  
 DB 169 ATEVTPVVPVTDYDGRGDSVVYGLRSKSKKFRFP 204  
 Query Match 54.4%; Score 181; DB 8; Length 218;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-12;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PN	WO2004013311-A2.	XX
PD	12-FEB-2004.	XX
PF	06-AUG-2003; 2003WO-US024669.	XX
PR	06-AUG-2002; 2002US-0401469P.	XX
PA	(DIAD-) DIADEXUS INC.	XX
PI	Macina RA, Salceda S, Liu C, Sun Y, Turner LR;	XX
WPI	2004-169331/16.	XX
PT	New ovarian specific nucleic acid, useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease states in ovarian tissue.	XX
PS	Claim 12; SEQ ID NO 390; 586pp; English.	XX
CC	The invention relates to novel isolated ovarian specific nucleic acid molecules and the polypeptides encoded by them. A protein of the invention has cytostatic and immunostimulant activity. A nucleic acid of the invention may have a use as a vaccine, and in gene therapy. The nucleic acid molecule or polypeptide, antibody or kit is useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non cancerous disease states in ovarian tissue and inducing an immune response against the ovarian cancer cell. The sequences shown in ADJ67535-ADJ67682 represent ovarian specific polypeptides of the invention.	XX
SEQ	Sequence 243 AA;	XX
Query Match	54.4%; Score 181; DB 8; Length 243;	
Best Local Similarity	97.2%; Pred. No. 3.2e-12;	
Matches	35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	5 ATEVTPVPVPTVDYDGRGDSVVYGRSKSKFRFP 40	
Db	71 ATEVTPVPVPTVDYDGRGDSVVYGLRSKSKFRFP 106	
RESULT 12		
AAO30815		
ID	AAO30815 standard; protein; 273 AA.	
XX		
AC	AAO30815;	
XX		
DT	22-SEP-2003 (first entry)	
XX		
DE	Human cell adhesion and extracellular matrix protein (CADECM)-5.	
XX		
KW	Human; cell adhesion and extracellular matrix protein; immune disorder;	
KW	CADECM; cancer; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003047526-A2.	
XX		
PD	12-JUN-2003.	
XX		
PF	26-NOV-2002; 2002WO-US038437.	
XX		
PR	30-NOV-2001; 2001US-0334343P.	
PR	07-DEC-2001; 2001US-0340278P.	
PR	04-JAN-2002; 2002US-0345069P.	
PR	25-JAN-2002; 2002US-0351352P.	
PR	14-FEB-2002; 2002US-0357168P.	
PR	29-MAR-2002; 2002US-0369128P.	
PR	05-APR-2002; 2002US-0370802P.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
XX		

RESULT 10		
ADJ67551		
ID	ADJ67551 standard; protein; 243 AA.	
XX		
AC	ADJ67551;	
XX		
DT	06-MAY-2004 (first entry)	
XX		
DE	Human ovarian specific polypeptide SEQ ID NO:265.	
XX		
KW	human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;	
KW	ovarian cancer; immune response; cancer.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004013311-A2.	
XX		
PD	12-FEB-2004.	
XX		
PF	06-AUG-2003; 2003WO-US024669.	
XX		
PR	06-AUG-2002; 2002US-0401469P.	
XX		
PA	(DIAD-) DIADEXUS INC.	
XX		
PI	Macina RA, Salceda S, Liu C, Sun Y, Turner LR;	
XX		
WPI	2004-169331/16.	
XX		
PT	New ovarian specific nucleic acid, useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease states in ovarian tissue.	
XX		
PS	Claim 12; SEQ ID NO 265; 586pp; English.	
XX		
CC	The invention relates to novel isolated ovarian specific nucleic acid molecules and the polypeptides encoded by them. A protein of the invention has cytostatic and immunostimulant activity. A nucleic acid of the invention may have a use as a vaccine, and in gene therapy. The nucleic acid molecule or polypeptide, antibody or kit is useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non cancerous disease states in ovarian tissue and inducing an immune response against the ovarian cancer cell. The sequences shown in ADJ67535-ADJ67682 represent ovarian specific polypeptides of the invention.	
XX		
SEQ	Sequence 243 AA;	
Query Match	54.4%; Score 181; DB 8; Length 243;	
Best Local Similarity	97.2%; Pred. No. 3.2e-12;	
Matches	35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	5 ATEVTPVPVPTVDYDGRGDSVVYGRSKSKFRFP 40	
Db	71 ATEVTPVPVPTVDYDGRGDSVVYGLRSKSKFRFP 106	
RESULT 11		
ADJ67676		
ID	ADJ67676 standard; protein; 243 AA.	
XX		
AC	ADJ67676;	
XX		
DT	06-MAY-2004 (first entry)	
XX		
DE	Human ovarian specific polypeptide SEQ ID NO:390.	
XX		
KW	human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;	
KW	ovarian cancer; immune response; cancer.	
XX		
OS	Homo sapiens.	
XX		

PI Baughn MR, Becha SD, Bhatia U, Blake JU, Borowsky ML, Burrill JD;  
 PI Deleage AM, Elliott VS, Gandhi AR, Gietzen KJ, Gorvad AE;  
 PI Griffin JA, Ho A, Jin P, Kable AE, Lal PG, Lee S, Lee SY;  
 PI Marquis JP, Lehn-Mason FM, Ramkumar J, Richardson TW, Sprague WW;  
 PI Swarnakar A, Tang TY, Tran B, Tran UK, Chawia NK, Warren BA, Xu Y;  
 XX Yue H, Zheng W;  
 DR WPI; 2003-513695/48.  
 DR N-PSDB; AAL62017.  
 XX  
 PT New human cell adhesion and extracellular matrix proteins (CADECM)  
 PT polypeptide, useful for preparing a composition for treating a disease  
 PT associated with decreased expression or overexpression of CADECM e.g.,  
 PT cancer.  
 XX  
 PS Claim 1; Page 277; 374pp; English.  
 XX  
 CC The invention relates to human cell adhesion and extracellular matrix  
 CC proteins (CADECM) and nucleic acid molecules encoding such proteins.  
 CC CADECM proteins are useful for preparing a composition for diagnosing or  
 CC treating a disease or condition associated with decreased expression or  
 CC overexpression of functional CADECM e.g., immune disorders or cancer. The  
 CC invention is also useful in gene therapy. The present sequence is human  
 CC CADECM protein  
 XX  
 SQ Sequence 273 AA;

Query Match 54.4%; Score 181; DB 7; Length 273;  
 Best Local Similarity 97.2%; Pred. No. 3.6e-12;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 40

DB 101 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 136

RESULT 13

ADM47287

ID ADM47287 standard; protein; 278 AA.

XX ADM47287;

XX 03-JUN-2004 (first entry)

XX Osteopontin like NOVX 11b protein.

XX NOVX; cytostatic; gene therapy; vaccine; cancer; chromosome mapping.

XX Unidentified.

XX WO2003083039-A2.

XX 09-OCT-2003.

XX 03-JUL-2002; 2002WO-US021485.

XX 05-JUL-2001; 2001US-0303046P.

XX 09-JUL-2001; 2001US-0303828P.

XX 11-JUL-2001; 2001US-0304502P.

XX 12-JUL-2001; 2001US-0305011P.

XX 13-JUL-2001; 2001US-0305262P.

XX 16-JUL-2001; 2001US-0305673P.

XX 17-JUL-2001; 2001US-0306085P.

XX 24-JUL-2001; 2001US-0307536P.

XX 27-JUL-2001; 2001US-0308228P.

XX 30-JUL-2001; 2001US-0308677P.

XX 14-AUG-2001; 2001US-0312203P.

XX 17-SEP-2001; 2001US-0322640P.

XX 19-SEP-2001; 2001US-0323484P.

XX 21-SEP-2001; 2001US-0323821P.

XX 21-SEP-2001; 2001US-0323948P.

XX 25-SEP-2001; 2001US-0324711P.

XX 09-OCT-2001; 2001US-0327893P.

PR 21-NOV-2001; 2001US-0331768P.  
 PR 21-FEB-2002; 2002US-0359191P.  
 PR 22-FEB-2002; 2002US-0358939P.  
 PR 28-FEB-2002; 2002US-0360923P.  
 PR 01-MAR-2002; 2002US-0360830P.  
 PR 01-MAR-2002; 2002US-0361178P.  
 PR 05-MAR-2002; 2002US-0361748P.  
 PR 12-MAR-2002; 2002US-0363429P.  
 PR 12-MAR-2002; 2002US-0363683P.  
 PR 12-MAR-2002; 2002US-0372141P.  
 PR 16-APR-2002; 2002US-0372967P.  
 PR 16-APR-2002; 2002US-0373051P.  
 PR 16-APR-2002; 2002US-0373063P.  
 PR 17-APR-2002; 2002US-0373280P.  
 PR 17-APR-2002; 2002US-0373287P.  
 PR 19-APR-2002; 2002US-0373881P.  
 PR 02-JUL-2002; 2002US-00187975.  
 XX  
 XX (CURA-) CURAGEN CORP.

XX Li L, Shenoy SG, Patturajan M, Ellerman K, Gorman L, Zhong M;

PI Catterton E, Spytek KA, Miller CE, Edinger SE, Hjalt T, Gerlach VL;

PI Shinkets RA, Taupier RJ, Anderson DW, Guo X, Baumgartner JC;

PI Padigaru M, Peyman JA, Smithson G, Casman SJ, Voss EZ, Boldog FL;

PI Pena CEA, Chapoval A, Raetelli L, Kekuda R, Vernet CM;

XX WPI; 2003-812538/76.

DR N-PSDB; ADM47286.

XX New NOVX polypeptide, useful for preparing a composition for treating or

PT preventing e.g. cancer or for chromosome mapping.

PT Claim 2; SEQ ID NO 120; 433pp; English.

XX The invention relates to a novel isolated polypeptide, designated NOVX.  
 CC The novel polypeptide comprises a sequence comprising 109-1671 amino  
 CC acids, or its mature form; a sequence that is at least 95% identical to  
 CC the 109-1671 amino acid polypeptide; or a sequence comprising one or more  
 CC conservative substitutions in the 109-1671 amino acid polypeptide. The  
 CC invention further comprises: a composition; a kit comprising the  
 CC polypeptide; a method for determining the presence or amount of the  
 CC polypeptide or nucleic acid molecule in a sample; determining the  
 CC presence of, or predisposition to, a disease associated with the altered  
 CC levels of nucleic acid or of expression of the polypeptide in a first  
 CC mammalian subject; identification of an agent that binds to the  
 CC polypeptide; identification of a potential therapeutic agent for treating  
 CC a pathology related to aberrant expression or physiological interactions  
 CC of the polypeptide; a method of screening for a modulator of activity or  
 CC latency of, or predisposition to, a pathology associated with the  
 CC polypeptide; a method for modulating the activity of the polypeptide;  
 CC treating or preventing a pathology associated with the polypeptide;  
 CC treating a pathological state in a mammal; an isolated nucleic acid  
 CC molecule; a vector comprising the nucleic acid molecule; a cell  
 CC comprising the vector; an antibody that immunospecifically binds to the  
 CC polypeptide; and a method for producing the polypeptide. The NOVX  
 CC polypeptide and its encoding nucleic acid have cytostatic activity. The  
 CC NOVX polynucleotide can be used in gene therapy to treat disorders. The  
 CC NOVX polypeptide can be used to create a vaccine. The polypeptide is  
 CC useful for preparing a composition for treating or preventing a  
 CC pathological state in a mammal, e.g., cancer, or for chromosome mapping.  
 CC This sequence represents a NOVX polypeptide of the invention.

XX Sequence 278 AA;

Query Match 54.4%; Score 181; DB 7; Length 278;

Best Local Similarity 97.2%; Pred. No. 3.7e-12;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 40

DB 128 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 163

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RESULT 14
ADSI0984
ID ADSI0984 standard; protein; 279 AA.
XX
AC ADSI0984;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic protein - SEQ ID 1221.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2004080148-A2.
XX
PD 23-SEP-2004.
XX
PF 30-SEP-2003; 2003WO-US030720.
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;
XX
DR WPI: 2004-668857/65.
DR N-PSDB; ADSI0300.
XX
PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
PS Claim 20; SEQ ID NO 1221; 718pp; English.
XX
CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 279 AA;
Query Match 54.4%; Score 181; DB 8; Length 279;
Best Local Similarity 97.2%; Pred. No. 3.7e-12;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
Db 115 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRPP 150
RESULT 15
AAR30701
ID AAR30701 standard; protein; 282 AA.
XX
AC AAR30701;
XX
DT 25-MAR-2003 (revised)
DT 14-MAY-1993 (first entry)
XX
DE Isoform of human osteopontin protein.
XX
KW Human; HUP; osteopontin; kidney stone; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO9222316-A1.
XX
PD 23-DEC-1992.
XX
PF 01-JUN-1992; 92WO-US004599.
XX
PR 10-JUN-1991; 91US-00712476.
XX
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA (UYPE-) UNIV PENNSYLVANIA.
PA (UYCA-) UNIV CAMBRIDGE.
XX
PI Hoyer J, Neilson E, Sinclair J, Clayman M, Shiraga H;
PI Borysiewicz L;
XX
DR WPI: 1993-017903/02.
XX
PT Compn. for treating kidney stone diseases, osteoporosis, etc. - contains
PT aspartic acid-rich protein, and proteins having homology of active
PT portions.
XX
PS Disclosure; Page 41; 65pp; English.
XX
CC To protein is an isoform of human osteopontin (see Young, et al.,
CC Genomics, Vol. 7, pp. 491-502, 1990). The last 4 amino acids of the HUP
CC sequences are deleted from the isoform encoded by mRNA from human bone,
CC decidua and kidney. The sequence may be used to design probes and primers
CC for the isolation of HUP DNA. See also AAR30700. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 282 AA;
Query Match 54.4%; Score 181; DB 2; Length 282;
Best Local Similarity 97.2%; Pred. No. 3.7e-12;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
Db 110 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRPP 145
Search completed: July 27, 2005, 18:11:55
Job time : 168 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 18:06:23 ; Search time 42 seconds  
(without alignments)  
111.974 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RRRATEVTPVPTVDYD.....ACGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181	54.4	282	1	US-07-712-476A-5
2	181	54.4	296	1	US-07-712-476A-1
3	181	54.4	300	4	US-09-949-016-5962
4	181	54.4	314	4	US-09-134-253-1
5	181	54.4	314	4	US-09-206-576-2
6	181	54.4	314	4	US-09-538-092-896
7	181	54.4	329	4	US-09-949-016-10363
8	177	53.2	300	6	5340934-6
9	177	53.2	300	6	5340934-6
10	160	48.0	32	4	US-09-134-253-6
11	118	35.4	278	6	5340934-8
12	118	35.4	278	6	5340934-8
13	111	33.3	317	4	US-09-485-077A-17
14	95.5	28.7	1057	3	US-08-931-820-1
15	95.5	28.7	1341	3	US-08-963-825-18
16	95.5	28.7	1341	3	US-09-500-811-18
17	95.5	28.7	1341	3	US-09-570-573-18
18	95.5	28.7	1341	3	US-09-548-608-18
19	95.5	28.7	1464	4	US-09-331-347C-21
20	91.5	27.5	1024	3	US-08-931-820-2
21	91.5	27.5	1366	3	US-08-963-825-19
22	91.5	27.5	1366	3	US-09-500-811-19
23	91.5	27.5	1366	3	US-09-570-573-19
24	91.5	27.5	1366	3	US-09-548-608-19
25	91.5	27.5	1366	4	US-09-585-887-10
26	91.5	27.5	1366	4	US-09-289-578-10
27	91.5	27.5	1366	4	US-09-949-016-5882

28	91.5	27.5	1461	4	US-09-585-887-9	Sequence 9, Appli
29	91.5	27.5	1461	4	US-09-289-578-9	Sequence 9, Appli
30	91.5	27.5	1516	4	US-09-949-016-8209	Sequence 8209, Ap
31	89	26.7	54	2	US-08-316-650-14	Sequence 14, Appl
32	89	26.7	54	5	PCT-US95-02251-14	Sequence 12731, A
33	89	26.7	435	4	US-09-902-540-12731	Sequence 10, Appl
34	89	26.7	1017	4	US-08-468-996-10	Sequence 3, Appli
35	89	26.7	1060	3	US-08-931-820-3	Sequence 20, Appl
36	89	26.7	1418	3	US-08-963-825-20	Sequence 1, Appli
37	89	26.7	1418	3	US-09-010-999-1	Sequence 1, Appli
38	89	26.7	1418	3	US-09-500-811-20	Sequence 20, Appl
39	89	26.7	1418	3	US-09-570-573-20	Sequence 20, Appl
40	89	26.7	1418	3	US-09-548-608-20	Sequence 20, Appl
41	89	26.7	1442	2	US-08-316-650-12	Sequence 12, Appl
42	89	26.7	1442	5	PCT-US95-02251-12	Sequence 12, Appl
43	87.5	26.3	279	3	US-09-010-999-2	Sequence 2, Appli
44	87.5	26.3	492	4	US-08-468-996-11	Sequence 11, Appl
45	87	26.1	308	3	US-08-956-307B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-07-712-476A-5  
; Sequence 5, Application US/07712476A  
; Patent No. 5304496  
; GENERAL INFORMATION:  
; APPLICANT: Hoyer et al.  
; TITLE OF INVENTION: Biological Regulation of  
; TITLE OF INVENTION: Mineralization  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
; ADDRESSEE: No. 5304496ris  
; STREET: One Liberty Place 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; OPERATING SYSTEM: PC DOS  
; SOFTWARE: WORDPERFECT 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07712,476A  
; FILING DATE: 19910610  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Suzanne E. Miller  
; REGISTRATION NUMBER: 32,279  
; REFERENCE/DOCKET NUMBER: UPN 0473  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568 3100  
; TELEFAX: (215) 568 3439  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 282 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
US-07-712-476A-5

Query Match 54.4%; Score 181; DB 1; Length 282;  
Best Local Similarity 97.2%; Pred No. 6.5e-13;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 ATEVFTPVVPTVDYDGRGDSVYVGRSKSKKFRFP 40  
Db 110 ATEVFTPVVPTVDYDGRGDSVYVGRSKSKKFRFP 145

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RESULT 2
US-07-712-476A-1
; Sequence 1, Application US/07712476A
; Patent No. 5304496
; GENERAL INFORMATION:
; APPLICANT: Hoyer et al.
; TITLE OF INVENTION: Biological Regulation of
; TITLE OF INVENTION: Mineralization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5304496ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07712,476A
; FILING DATE: 19910610
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Suzanne E. Miller
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN 0473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568 3100
; TELEFAX: (215) 568 3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-712-476A-1

Query Match 54.4%; Score 181; DB 1; Length 296;
Best Local Similarity 97.2%; Pred. No. 6.9e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
|||||
Db 124 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 159

RESULT 3
US-09-949-016-5962
; Sequence 5962, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5962
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5962

Query Match 54.4%; Score 181; DB 4; Length 300;
Best Local Similarity 97.2%; Pred. No. 7e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
|||||
Db 128 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 163

RESULT 4
US-09-134-253-1
; Sequence 1, Application US/09134253
; Patent No. 6509026
; GENERAL INFORMATION:
; APPLICANT: Ashkar, Sammy
; TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
; FILE REFERENCE: cme-100cp
; CURRENT APPLICATION NUMBER: US/09/134,253
; CURRENT FILING DATE: 1998-08-14
; EARLIER APPLICATION NUMBER: 08/916,912
; EARLIER FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-134-253-1

Query Match 54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
|||||
Db 142 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 177

RESULT 5
US-09-206-576-2
; Sequence 2, Application US/09206576
; Patent No. 6551990
; GENERAL INFORMATION:
; APPLICANT: Giachelli, Cecilia M.
; APPLICANT: Steitz, Susie
; TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification
; FILE REFERENCE: P-UW 3244
; CURRENT APPLICATION NUMBER: US/09/206,576
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-576-2

Query Match 54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
|||||
Db 142 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 177

RESULT 6
US-09-206-576-2

Query Match 54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
|||||
Db 142 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 177

RESULT 6
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```
US-09-538-092-896
; Sequence 896, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormat Version 0.9
; SEQ ID NO 896
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P10451
; US-09-538-092-896

Query Match      54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 40
|||||:|||||:|||||:|||||:|||||:|||||:
Db 142 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 177

RESULT 7
US-09-949-016-10363
; Sequence 10363, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10363
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10363

Query Match      54.4%; Score 181; DB 4; Length 329;
Best Local Similarity 97.2%; Pred. No. 7.7e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 40
|||||:|||||:|||||:|||||:|||||:|||||
Db 157 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 192

RESULT 8
5340934-6
; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
```

```
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:6;
; LENGTH: 300
5340934-6

Query Match      53.2%; Score 177; DB 6; Length 300;
Best Local Similarity 94.4%; Pred. No. 2e-12;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 40
|||||:|||||:|||||:|||||:|||||:|||||
Db 128 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 163

RESULT 9
5340934-6
; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:6;
; LENGTH: 300
5340934-6

Query Match      53.2%; Score 177; DB 6; Length 300;
Best Local Similarity 94.4%; Pred. No. 2e-12;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 40
|||||:|||||:|||||:|||||:|||||:|||||
Db 128 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 163

RESULT 10
US-09-134-253-6
; Sequence 6, Application US/09134253
; Patent No. 6509026
; GENERAL INFORMATION:
; APPLICANT: Ashkar, Sammy
; TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
; FILE REFERENCE: cme-100cp
; CURRENT APPLICATION NUMBER: US/09/134,253
; CURRENT FILING DATE: 1998-08-14
; EARLIER APPLICATION NUMBER: 08/916,912
; EARLIER FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-134-253-6

Query Match      48.0%; Score 160; DB 4; Length 32;
Best Local Similarity 96.9%; Pred. No. 1.4e-11;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 39
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Db 1 VFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 32

RESULT 11
5340934-8
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; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.:YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:8:
; LENGTH: 278
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Query Match          35.4%; Score 118; DB 6; Length 278;
Best Local Similarity 68.8%; Pred. No. 9.2e-06;
Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY      8 VFTPVVPTVDTYDGRGDSVVYGRRSKSKKFR 39
DB     138 VFTPIPTESANDGRGDSVAYGLKRSKKFR 169

RESULT 12
5340934-8
; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.:YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:8:
; LENGTH: 278
5340934-8
Query Match          35.4%; Score 118; DB 6; Length 278;
Best Local Similarity 68.8%; Pred. No. 9.2e-06;
Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY      8 VFTPVVPTVDTYDGRGDSVVYGRRSKSKKFR 39
DB     138 VFTPIPTESANDGRGDSVAYGLKRSKKFR 169

RESULT 13
US-09-485-077A-17
; Sequence 17, Application US/09485077A
; Patent No. 6458590
; GENERAL INFORMATION:
; APPLICANT: Mukherjee, Anil
; APPLICANT: Kundu, Gopal
; APPLICANT: Panda, Dibyendu
; TITLE OF INVENTION: Methods and Compositions for Treatment of Restenosis
; FILE REFERENCE: NIH-05047
; CURRENT APPLICATION NUMBER: US/09/485,077A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/US98/16569
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: 60/054,967
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Rattus No. 6458590vegicus
US-09-485-077A-17
Query Match          33.3%; Score 111; DB 4; Length 317;
Best Local Similarity 64.5%; Pred. No. 6.6e-05;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY      7 EVFTPVVPTVDTYDGRGDSVVYGRRSKSKKF 37
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DB     129 DVLPIAPTVDVDPGRGDSLAYGLRSKRSF 159

RESULT 14
US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Assay for collagen degradation
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96202596.1
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Collagen type I
US-08-931-820-1
Query Match          28.7%; Score 95.5; DB 3; Length 1057;
Best Local Similarity 65.5%; Pred. No. 0.015;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;
QY      40 PAGAG-----GPAGPAGPAGPAGPAGPA 63
DB     898 PAGSGDRGETGPAGPAGPAGPAGPAGPA 926

RESULT 15
US-08-963-825-18
; Sequence 18, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
; APPLICANT: Oviat, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,825
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; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GOGORIS, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1341 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN ALPHA 1 (I)
; US-08-963-825-18

Query Match      28.7%; Score 95.5; DB 3; Length 1341;
Best Local Similarity 65.5%; Pred. No. 0.019; 4; Indels 5; Gaps 1;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY      40  PACAAG-----GPAGPAGPAGPAGPAGPA 63
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Db      935  PAGKSGDRGTGTGTPAGPAGPAGPAGPAGPA 963

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:14:59 ; Search time 154 Seconds  
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159.133 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	236	70.9	87	15	US-10-220-107-6
2	236	70.9	87	17	US-10-900-512-6
3	181	54.4	192	9	US-09-805-020-41
4	181	54.4	278	15	US-10-187-975-120
5	181	54.4	286	16	US-10-477-876-3
6	181	54.4	287	14	US-10-097-340-231
7	181	54.4	287	14	US-10-171-311-176
8	181	54.4	287	14	US-10-205-823-307
9	181	54.4	287	14	US-10-177-293-340
10	181	54.4	287	14	US-10-301-822-147
11	181	54.4	287	16	US-10-678-355-6
					Sequence 6, Appli

12	181	54.4	290	15	US-10-187-975-48	Sequence 48, Appli
13	181	54.4	299	16	US-10-477-876-2	Sequence 2, Appli
14	181	54.4	300	9	US-09-919-770-2	Sequence 229, App
15	181	54.4	300	14	US-10-097-340-229	Sequence 174, App
16	181	54.4	300	14	US-10-171-311-174	Sequence 305, App
17	181	54.4	300	14	US-10-205-823-305	Sequence 338, App
18	181	54.4	300	14	US-10-177-293-338	Sequence 145, App
19	181	54.4	300	14	US-10-301-822-145	Sequence 267, App
20	181	54.4	300	15	US-10-170-385-267	Sequence 508, App
21	181	54.4	300	15	US-10-295-027-508	Sequence 1333, Ap
22	181	54.4	300	15	US-10-087-080-12	Sequence 12, Appli
23	181	54.4	300	15	US-10-087-080-12	Sequence 15, Appli
24	181	54.4	300	15	US-10-229-345-15	Sequence 15, Appli
25	181	54.4	300	15	US-10-274-177-15	Sequence 15, Appli
26	181	54.4	300	16	US-10-650-112-15	Sequence 4, Appli
27	181	54.4	300	16	US-10-678-355-4	Sequence 8, Appli
28	181	54.4	300	16	US-10-764-649-8	Sequence 75, Appli
29	181	54.4	300	16	US-10-734-564-75	Sequence 31, Appli
30	181	54.4	300	17	US-10-690-880-31	Sequence 22, Appli
31	181	54.4	300	17	US-10-818-066-22	Sequence 42, Appli
32	181	54.4	300	18	US-10-849-989-42	Sequence 90, Appli
33	181	54.4	300	18	US-10-712-124-90	Sequence 2, Appli
34	181	54.4	314	9	US-09-206-576-2	Sequence 24, Appli
35	181	54.4	314	10	US-09-983-000A-24	Sequence 227, App
36	181	54.4	314	14	US-10-097-340-227	Sequence 172, App
37	181	54.4	314	14	US-10-171-311-172	Sequence 1, Appli
38	181	54.4	314	14	US-10-303-583-1	Sequence 303, App
39	181	54.4	314	14	US-10-205-823-303	Sequence 336, App
40	181	54.4	314	14	US-10-177-293-336	Sequence 60, Appli
41	181	54.4	314	14	US-10-241-220-60	Sequence 143, App
42	181	54.4	314	14	US-10-301-822-143	Sequence 2, Appli
43	181	54.4	314	14	US-10-376-383-2	Sequence 1, Appli
44	181	54.4	314	14	US-10-239-555A-1	Sequence 1, Appli
45	181	54.4	314	15	US-10-220-107-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-10-220-107-6  
; Sequence 6, Application US/10220107  
; Publication No. US20040034193A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkar, Samy  
; APPLICANT: Hikita, Sherry  
; APPLICANT: Dehnl, Ghassan  
; TITLE OF INVENTION: Biosynthetic Oncolytic Molecules and Uses Therefor  
; FILE REFERENCE: CMCC 725  
; CURRENT APPLICATION NUMBER: US/10/220,107  
; CURRENT FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 6  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-220-107-6

Query Match 70.9%; Score 236; DB 15; Length 87;  
Best Local Similarity 86.8%; Pred. No. 4.4e-17;  
Matches 46; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 10 TPVPTVTDYDGRGDSVYVGRRSKSKFRRPAGAGGAGPAGPAGPAGP 62  
Db 41 TPVPTVTDYDGRGDSVYVGLRSK-----PAGAGGAGPAGPAGPAGP 87

RESULT 2  
US-10-900-512-6  
; Sequence 6, Application US/10900512

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; Publication No. US20050048614A1
; GENERAL INFORMATION:
; APPLICANT: Ashkar, Samy
; APPLICANT: Hikota, Sherry
; APPLICANT: Dehai, Ghassan
; TITLE OF INVENTION: Biosynthetic Oncolytic Molecules and Uses Thereof
; FILE REFERENCE: CMCC 725 CIP
; CURRENT APPLICATION NUMBER: US/10/900,512
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: 60/491,775
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/220,107
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US01/19239
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,436
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-900-512-6

Query Match 70.9%; Score 236; DB 17; Length 87;
Best Local Similarity 86.8%; Pred. No. 4.4e-17;
Matches 46; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 10 TPVFTPTVDYDGRGDSVVYGRSKKKFRPAGAGGPGAGPGAGPAGP 62
Db 41 TPVFTPTVDYDGRGDSVVYGLRSK-----PAGAAGGPGAGPGAGPAGP 87

RESULT 3
US-09-805-020-41
; Sequence 41, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-020-41

Query Match 54.4%; Score 181; DB 9; Length 192;
Best Local Similarity 97.2%; Pred. No. 5.2e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKKKFRP 40
Db 142 ATEVFTPVVPTVDYDGRGDSVVYGLRSKKKFRP 177

RESULT 4
US-10-187-975-120
; Sequence 120, Application US/10187975
; Publication No. US2003024982A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Sheno, Suresh
; APPLICANT: Patturajan, Meera
; APPLICANT: Ellerman, Karen
; APPLICANT: Gorman, Linda
```

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; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Spytek, Kimberly
; APPLICANT: Miller, Charles
; APPLICANT: Edinger, Shlomit
; APPLICANT: Hjalt, Tord
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Baumgartner, Jason
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Pena, Carol
; APPLICANT: Chapoval, Andrei
; APPLICANT: Rastelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Vernte, Corine
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: 21402-397A
; CURRENT APPLICATION NUMBER: US/10/187,975
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303,046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/303,828
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/304,502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305,011
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,262
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/305,673
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/306,085
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/307,536
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/308,228
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/308,877
; PRIOR FILING DATE: 2001-07-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 120
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-187-975-120

Query Match 54.4%; Score 181; DB 15; Length 278;
Best Local Similarity 97.2%; Pred. No. 7.6e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKKKFRP 40
Db 128 ATEVFTPVVPTVDYDGRGDSVVYGLRSKKKFRP 163

RESULT 5
US-10-477-876-3
; Sequence 3, Application US/10477876
; Publication No. US20040235720A1
; GENERAL INFORMATION:
; APPLICANT: Applied Research Systems ARS Holding N.V.
; TITLE OF INVENTION: Use of osteopontin for the treatment and/or prevention of demyelination
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; TITLE OF INVENTION: diseases
; FILE REFERENCE: WO 473
; CURRENT APPLICATION NUMBER: US/10/477,876
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 0111296
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-477-876-3

Query Match      54.4%; Score 181; DB 16; Length 286;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 40
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Db 114 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 149

RESULT 6
US-10-097-340-231
; Sequence 231, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHWANDT
; APPLICANT: Xumel ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-231

Query Match      54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 40
    |||||
Db 115 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 150

RESULT 7
US-10-171-311-176
; Sequence 176, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-176

Query Match      54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKKFRPP 40
    |||||
Db 115 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKKFRPP 150

RESULT 8
US-10-205-823-307
; Sequence 307, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25

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; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 307
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-307

Query Match          54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRFP 40
    |||||
Db 115 ATEVFTPVVPTVDTYDGRGDSVYGLRSKSKKFRFP 150

RESULT 9
US-10-177-293-340
; Sequence 340, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Fustai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-340
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Query Match          54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRFP 40
    |||||
Db 115 ATEVFTPVVPTVDTYDGRGDSVYGLRSKSKKFRFP 150

RESULT 10
US-10-301-822-147
; Sequence 147, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-147

Query Match          54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVYGRRSKSKKFRFP 40
    |||||
Db 115 ATEVFTPVVPTVDTYDGRGDSVYGLRSKSKKFRFP 150

RESULT 11
US-10-678-355-6
; Sequence 6, Application US/10678355
; Publication No. US20040142865A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Georg F.
; TITLE OF INVENTION: OSTEOPONTIN-BASED CANCER THERAPIES
; FILE REFERENCE: 00398-148001
; CURRENT APPLICATION NUMBER: US/10/678,355
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,712
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-678-355-6

Query Match          54.4%; Score 181; DB 16; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
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Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRRSKSKKFRFP 40  
|||||  
Db 115 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 150  
|||||

## RESULT 12

US-10-187-975-48  
; Sequence 48, Application US/10187975  
; Publication No. US20030224982A1  
; GENERAL INFORMATION:

; APPLICANT: Li, Li  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Gorman, Linda  
; APPLICANT: Zhong, Mei  
; APPLICANT: Catterton, Elina  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Miller, Charles  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Hjalte, Tord  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Taupier, Raymond J. Jr.  
; APPLICANT: Anderson, David  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Peyman, John  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Casman, Stacie  
; APPLICANT: Voss, Edward  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Fena, Carol  
; APPLICANT: Chapoval, Andrei  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Vernte, Corine

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: 21402-397A  
; CURRENT APPLICATION NUMBER: US/10/187,975  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/303,046  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/303,828  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/304,502  
; PRIOR FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 60/305,011  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/305,262  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/305,673  
; PRIOR FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/306,085  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 60/307,536  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/308,228  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/308,877  
; PRIOR FILING DATE: 2001-07-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 288

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 48

; LENGTH: 290

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-187-975-48

Query Match 54.4%; Score 181; DB 15; Length 290;  
Best Local Similarity 97.2%; Pred. No. 7.9e-11;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRRSKSKKFRFP 40  
|||||  
Db 142 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 177  
|||||

## RESULT 13

US-10-477-876-2  
; Sequence 2, Application US/10477876  
; Publication No. US20040235720A1  
; GENERAL INFORMATION:

; APPLICANT: Applied Research Systems ARS Holding N.V.  
; TITLE OF INVENTION: Use of osteopontin for the treatment and/or prevention of demyel

; FILE REFERENCE: WO 473

; CURRENT APPLICATION NUMBER: US/10/477,876

; CURRENT FILING DATE: 2003-11-17

; PRIOR APPLICATION NUMBER: 01111296

; PRIOR FILING DATE: 2001-05-17

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 299

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-477-876-2

Query Match 54.4%; Score 181; DB 16; Length 299;  
Best Local Similarity 97.2%; Pred. No. 8.1e-11;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRRSKSKKFRFP 40  
|||||  
Db 127 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 162  
|||||

## RESULT 14

US-09-919-770-2  
; Sequence 2, Application US/09919770  
; Patent No. US20020048577A1  
; GENERAL INFORMATION:

; APPLICANT: Bornstein, Paul

; APPLICANT: Kyriakides, Themis

; APPLICANT: Ratner, Buddy

; APPLICANT: Giachelli, Cecilia

; APPLICANT: Martinson, Laura

; APPLICANT: Scatena, Marta

; TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response  
; FILE REFERENCE: UOPW117618

; CURRENT APPLICATION NUMBER: US/09/919,770

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,071

; PRIOR FILING DATE: 2000-08-01

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-919-770-2

Query Match 54.4%; Score 181; DB 9; Length 300;  
Best Local Similarity 97.2%; Pred. No. 8.2e-11;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRRSKSKKFRFP 40  
|||||  
Db 128 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 163  
|||||

```
RESULT 15
US-10-097-340-229
; Sequence 229, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 229
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-229
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Query Match      54.4%; Score 181; DB 14; Length 300;
Best Local Similarity 97.2%; Pred. No. 8.2e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
      |||||
Db      128 ATEVETPVVPTVDTYDGRGDSVVYGLRSKSKKFRPP 163
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Search completed: July 27, 2005, 18:28:26  
Job time : 155 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 18:05:17 ; Search time 39 Seconds  
(without alignments)  
155.427 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RSRATEVFTPVVPTVDTYD.....AGGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	181	54.4	314	1	S09575	osteopontin precur
2	128.5	38.6	303	1	GEPC0	osteopontin precur
3	121.5	36.5	311	1	JC1191	osteopontin precur
4	118	35.4	278	1	JS0638	probable tail fibe
5	114	34.2	407	2	G90907	osteopontin - rat
6	113	33.9	294	1	A37818	osteopontin precur
7	111	33.3	301	2	JCS811	osteopontin precur
8	111	33.3	317	1	A25917	collagen short cha
9	107.5	32.3	366	2	S11449	collagen 13, nonfi
10	107.5	32.3	423	2	A41207	hypothetical prote
11	98	29.4	1039	2	T35878	probable tail fibe
12	97	29.1	437	2	H90854	probable tail fibe
13	97	29.1	439	2	C90769	probable tail fibe
14	96	28.8	1464	2	S59856	collagen alpha 1(I
15	95.5	28.7	1464	1	CGHU1S	collagen alpha 1(I
16	95.5	28.7	1486	1	B40333	hypothetical prote
17	95	28.5	283	2	T32921	hypothetical prote
18	95	28.5	294	2	T29838	probable tail fibe
19	94	28.2	437	2	H90877	probable tail fibe
20	94	28.2	437	2	E90996	probable tail fibe
21	94	28.2	439	2	A85719	probable tail fibe
22	94	28.2	439	2	A85741	hypothetical prote
23	93	27.9	283	2	T29837	hypothetical prote
24	93	27.9	294	2	T29839	hypothetical prote
25	93	27.9	375	2	G85631	hypothetical prote
26	93	27.9	423	2	C78434	SLH family protein
27	93	27.9	437	2	E90968	probable tail fibe
28	93	27.9	438	2	S53787	collagen alpha cha
29	93	27.9	439	2	E85816	probable tail fibe

ALIGNMENTS

RESULT 1

S09575

osteopontin precursor, splice form A - human

N:Alternate names: bone sialoprotein I; lactopontin; milk protein, 75K; secreted phosph

N:Contains: osteopontin, splice form B; osteopontin, splice form C

C:Species: Homo sapiens (man)

C>Date: 20-May-1994 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004

C:Accession: S50028; S09575; A35326; JQ1529; I56986; I76601; I76602; A41802; S04505

R:Hiijiya, N.; Setoguchi, M.; Matsuura, K.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.

Biochem. J. 303, 255-262, 1994

A>Title: Cloning and characterization of the human osteopontin gene and its promoter.

A:Reference number: S50028, MUID:95031968; PMID:7945249

A:Accession: S50028

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-314 <HIJ>

A:Cross-references: UNIPROT:PI0451; EMBL:D14813; NID:G506341; PIDN:BAA03554.1; PID:G506

A>Note: The authors translated the codon GTG for residue 5 as Tyr

R:Kiefer, M.C.; Bauer, D.M.; Barr, P.J.

Nucleic Acids Res. 17, 3306, 1989

A>Title: The cDNA and derived amino acid sequence for human osteopontin.

A:Reference number: S09575, MUID:89263749; PMID:2726470

A:Accession: S09575

A:Molecule type: mRNA

A:Residues: 1-314 <KIE>

A:Cross-references: EMBL:X13694; NID:G35147; PIDN:CAA31984.1; PID:G35148

R:Young, M.F.; Kerr, J.M.; Termini, J.D.; Wewer, U.M.; Ge Wang, M.; McBride, O.W.; Fish

Genomics 7, 491-502, 1990

A>Title: cDNA cloning, mRNA distribution and heterogeneity, chromosomal location, and R

A:Reference number: A35326; MUID:90353945; PMID:1974876

A:Accession: A35326

A:Molecule type: mRNA

A:Residues: 1-58,73-314 <YOU>

A:Cross-references: GB:J04765; NID:G189404; PIDN:AAA59974.1; PID:G189405

R:Kohri, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Amasaki, N.; Yamate, T.; Umekawa, T.

Biochem. Biophys. Res. Commun. 184, 859-864, 1992

A>Title: Molecular cloning and sequencing of cDNA encoding urinary stone protein, which

A:Reference number: JQ1529; MUID:92246977; PMID:1575754

A:Accession: JQ1529

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 67-273 <KOH>

A:Experimental source: kidney

R:Saitoh, Y.; Kuratsu, J.; Takeshima, H.; Yamamoto, S.; Ushio, Y.

Lab. Invest. 72, 55-63, 1995

A>Title: Expression of osteopontin in human glioma. Its correlation with the malignancy

A:Reference number: I56986; MUID:95139605; PMID:7837791

A:Accession: I56986

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-187,'H',189-236,'A',238-314 <SAII>

A:Cross-references: GB:D28759; NID:G633074; PIDN:BAA05949.1; PID:G992948

A:Accession: I76601  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-57,72-187,'H',189-236,'A',238-314 <SAI2>  
A:Cross-references: GB:D28760; NID:g633075; PIDN:BAA05950.1; PID:g992949  
A:Accession: I76602  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-31,59-187,'H',189-236,'A',238-314 <SAI3>  
A:Cross-references: GB:D28761; NID:g633076; PIDN:BAA05951.1; PID:g992950  
R:Shraga, H.; Min, W.; VanDusen, W.J.; Clayman, M.D.; Miner, D.; Terrell, C.H.; Sherbot  
Proc. Natl. Acad. Sci. U.S.A. 89, 426-430, 1992  
A:Title: Inhibition of calcium oxalate crystal growth in vitro by uropontin: another mem  
A:Reference number: A41802; MUID:92108068; PMID:1729712  
A:Accession: A41802  
A:Molecule type: protein  
A:Residues: 19-62 <SHI>  
R:Senger, D.R.; Perruzzi, C.A.; Papadopoulos, A.; Tenen, D.G.  
Biochim. Biophys. Acta 996, 43-48, 1989  
A:Title: Purification of a human milk protein closely similar to tumor-secreted phosphop  
A:Reference number: S04505; MUID:89287357; PMID:2736258  
A:Accession: S04505  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 17-23;169-182 <SEN>  
A:Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,  
C:Genetics:  
A:Gene: GDB:SPPI; BNSP; OPN  
A:Cross-references: GDB:118889; OMIM:166490  
A:Map position: 4q21-q25  
C:Superfamily: osteopontin  
C:Keywords: alternative splicing; bone; cell binding; extracellular matrix; phosphoprote  
F:1-314/Product: osteopontin precursor, splice form A #status predicted <PRA>  
F:1-57,72-314/Product: osteopontin precursor, splice form B #status predicted <PRB>  
F:1-31,59-314/Product: osteopontin precursor, splice form C #status predicted <PRC>  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-314/Product: osteopontin #status predicted <MAT>  
F:86-95/Region: aspartic acid-rich  
F:159-161/Region: cell attachment (R-G-D) motif  
F:24,26,27,62,63,191,234,303,308,310/Binding site: phosphate (Ser) (covalent) #statu  
F:79,106/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:185/Binding site: phosphate (Thr) (covalent) #status predicted  
Query Match 54.4%; Score 181; DB 1; Length 314;  
Best Local Similarity 97.2%; Pred. No. 1.2e-10;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKFRP 40  
DB 142 ATEVFTPVVPTVDTYDGRGDSVVYGLURSKSKFRP 177  
RESULT 2  
GEPGO  
osteopontin precursor - pig  
N:Alternate names: bone sialoprotein I; phosphoprotein I, secreted  
N:Contains: 20K glycoprotein; 23K glycoprotein  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text\_change 09-Jul-2004  
C:Accession: S14903; A35204; S24372; S06690  
R:Wrana, J.L.; Zhang, Q.; Sodek, J.  
Nucleic Acids Res. 17, 10119, 1989  
A:Title: Full length cDNA sequence of porcine secreted phosphoprotein-I (SPP-I, osteopon  
A:Reference number: S14903; MUID:90098793; PMID:2602123  
A:Accession: S14903  
A:Molecule type: mRNA  
A:Residues: 1-303 <WRA>  
A:Cross-references: UNIPROT:P14287; EMBL:X16575; NID:g2120; PIDN:CAA34594.1; PID:g2121  
R:Zhang, Q.; Domenicucci, C.; Goldberg, H.A.; Wrana, J.L.; Sodek, J.  
J. Biol. Chem. 265, 7583-7589, 1990  
A:Title: Characterization of fetal porcine bone sialoproteins, secreted phosphoprotein I  
is derived from the carboxyl terminus of SPP-I.  
A:Reference number: A35204; MUID:90237064; PMID:2332443

A:Accession: A35204  
A:Molecule type: protein  
A:Residues: 17-36;172-211 <ZHA>  
R:Zhang, Q.; Wrana, J.L.; Sodek, J.  
Eur. J. Biochem. 207, 649-659, 1992  
A:Title: Characterization of the promoter region of the porcine opn (osteopontin, secret  
omoter.  
A:Reference number: S24372; MUID:92339454; PMID:1633816  
A:Accession: S24372  
A:Molecule type: DNA  
A:Residues: 1-18 <ZHA>  
A:Cross-references: EMBL:M84121; NID:g164599; PIDN:AAA31094.1; PID:g164600  
C:Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,  
C:Superfamily: osteopontin  
C:Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-303/Product: osteopontin #status experimental <MAT>  
F:86-93/Region: aspartic acid-rich  
F:154-156/Region: cell attachment (R-G-D) motif  
F:172-303/Product: 23K glycoprotein #status experimental <23K>  
F:193-303/Product: 20K glycoprotein #status experimental <20K>  
F:79/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 38.6%; Score 128.5; DB 1; Length 303;  
Best Local Similarity 80.0%; Pred. No. 1.6e-05;  
Matches 28; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKFR 39  
DB 138 ATDV-TPAVPTGDPNDGRGDSVVYGLURSKSKFR 171  
RESULT 3  
JC1191  
osteopontin precursor - rabbit  
N:Alternate names: bone sialoprotein I; secreted phosphoprotein I  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: JC1191; S54977; S54976  
R:Tezuka, K.; Sato, T.; Kamioka, H.; Nijweide, P.J.; Tanaka, K.; Matsuo, T.; Ohta, M.;  
Biochem. Biophys. Res. Commun. 186, 911-917, 1992  
A:Title: Identification of osteopontin in isolated rabbit osteoclasts.  
A:Reference number: JC1191; MUID:92360044; PMID:1379809  
A:Accession: JC1191  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-311 <TEZ>  
A:Cross-references: UNIPROT:P31097; DDBJ:D11411; NID:g217735; PIDN:BAA01993.1; PID:g2177  
A:Note: the authors translated the codon TCT for residue 126 as Glu and GAC for residue  
R:Nasu, K.; Ishida, T.; Setoguchi, M.; Higuchi, Y.; Akiyuki, S.; Yamamoto, S.  
Biochem. J. 307, 257-265, 1995  
A:Title: Expression of wild-type and mutated rabbit osteopontin in Escherichia coli, an  
A:Reference number: S54977; MUID:95234045; PMID:7717985  
A:Accession: S54977  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 78-84,'V',86-99,'Q',101-128,'SDE',129-150,'I',152-166 <NAS>  
A:Cross-references: EMBL:D16544  
R:Nasu, K.; Ishida, T.; Hijiya, N.; Setoguchi, M.; Akiyuki, S.; Higuchi, Y.; Yamamoto, T.  
submitted to the EMBL Data Library, September 1994  
A:Description: Molecular cloning of rabbit osteopontin cDNA and its expression.  
A:Reference number: S54976  
A:Accession: S54976  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-84,'V',86-99,'Q',101-128,'SDE',129-150,'I',152-311 <NA2>  
A:Cross-references: EMBL:D16544; NID:g538244; PIDN:BAA03980.1; PID:g538245  
C:Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,  
C:Genetics:  
A:Gene: OC-1  
C:Superfamily: osteopontin  
C:Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein  
F:1-16/Domain: signal sequence #status predicted <SIG>

C;Accession: G90907

A;Residues: 1-42, 'P', 44-294 <PAT>  
A;Cross-references: EMBL:X16151; NID:g50863; PIDN:CRA34276.1; PID:g50864  
R;Singh, R.P.; Patarica, R.; Schwartz, J.; Singh, P.; Cantor, H.  
J. Exp. Med. 171, 1931-1942, 1990  
A;Title: Definition of a specific interaction between the early T lymphocyte activation  
A;Reference number: A60931; MUID:90278349; PMID:2351930  
A;Accession: A60931  
A;Molecule type: protein  
A;Residues: 158-176 <SIN>  
A;Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,  
C;Genetics:  
A;Gene: Eta-1  
A;Map position: 5  
A;Introns: 18/3; 30/3; 57/3; 71/3; 165/3  
C;Superfamily: osteopontin  
C;Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-294/Product: osteopontin #status predicted <MAT>  
F;85-96/Region: aspartic acid-rich  
F;144-146/Region: cell attachment (R-G-D) motif  
F;78/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.9%; Score 113; DB 1; Length 294;  
Best Local Similarity 62.5%; Pred. No. 0.00052;  
Matches 20; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 7 EVFTPVPTVDYDGRGDSVYGRSKSKKF 38  
: |||:|||||:|||||:|||||:|  
Db 129 DFTFTPIPTVDVDPNGRDSLAYGLRSKRSF 160

RESULT 7  
JC5811  
osteopontin - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 07-May-1999  
C;Accession: JC5811  
R;Lasa, M.; Chang, P.L.; Prince, C.W.; Pinna, L.A.  
Biochem. Biophys. Res. Commun. 240, 602-605, 1997  
A;Title: Phosphorylation of osteopontin by Golgi apparatus casein kinase.  
A;Reference number: JC5811; MUID:98063283; PMID:9398611  
A;Accession: JC5811  
A;Molecule type: protein  
A;Residues: 1-301 <LAS>  
A;Experimental source: brain  
C;Comment: This protein is involved in the initiation of the bone calcification process,  
ues, early resistance to bacterial infection and binding of tumor cells at secondary site  
C;Superfamily: osteopontin

Query Match 33.3%; Score 111; DB 2; Length 301;  
Best Local Similarity 64.5%; Pred. No. 0.00083;  
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 7 EVFTPVPTVDYDGRGDSVYGRSKSKKF 37  
: |||:|||||:|||||:|||||:|  
Db 113 DVLTPAIPTVDVDPGRGDSLAYGLRSKRSF 143

RESULT 8  
A25917  
osteopontin precursor - rat  
N;Alternate names: bone sialoprotein I; phosphoprotein I, secreted; tumor-secreted phosph  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 18-Dec-1987 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
C;Accession: A25917; A45132; S28772; S04506; A45925  
R;Oldberg, A.; Franzen, A.; Heinegard, D.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8819-8823, 1986  
A;Title: Cloning and sequence analysis of rat bone sialoprotein (osteopontin) cDNA revea  
A;Reference number: A25917; MUID:87067405; PMID:3024151  
A;Accession: A25917  
A;Molecule type: mRNA  
A;Residues: 1-317 <OLD>  
A;Cross-references: UNIPROT:P08721; GB:M14656; NID:g205859; PIDN:AAA41762.1; PID:g205860

R;Singh, K.; Mukherjee, A.B.; De Vouge, M.W.; Mukherjee, B.B.  
J. Biol. Chem. 267, 23847-23851, 1992  
A;Title: Differential processing of osteopontin transcripts in rat kidney- and osteoblas  
A;Reference number: A45132; MUID:93054745; PMID:1429723  
A;Accession: A45132  
A;Molecule type: protein  
A;Residues: 36-51 <SIN1>  
A;Experimental source: kidney  
A;Note: sequence extracted from NCBI backbone (NCBIP:118869)  
A;Accession: B45132  
A;Molecule type: protein  
A;Residues: 272-282 <SIN2>  
A;Note: sequence extracted from NCBI backbone (NCBIP:118871)  
R;Prince, C.W.; Oosawa, T.; Butler, W.T.; Tomana, M.; Bhowm, A.S.; Bhowm, M.; Schrohenlo  
J. Biol. Chem. 262, 2900-2907, 1987  
A;Title: Isolation, characterization, and biosynthesis of a phosphorylated glycoprotein  
A;Reference number: S28772; MUID:87137549; PMID:3469201  
A;Accession: S28772  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 17-26, 'X' <PRI>  
R;Senger, D.R.; Perruzzi, C.A.; Papadopoulos, A.; Tenen, D.G.  
Biochim. Biophys. Acta 996, 43-48, 1989  
A;Title: Purification of a human milk protein closely similar to tumor-secreted phosphop  
A;Reference number: S04505; MUID:89287357; PMID:2736258  
A;Accession: S04506  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 17-26,155-167 <SEN>  
R;Senger, D.R.; Perruzzi, C.A.; Gracey, C.F.; Papadopoulos, A.; Tenen, D.G.  
Cancer Res. 48, 5770-5774, 1988  
A;Title: Secreted phosphoproteins associated with neoplastic transformation: close homol  
A;Reference number: A45925; MUID:89002730; PMID:3167835  
A;Accession: A45925  
A;Molecule type: protein  
A;Residues: 17-25 <SE2>  
C;Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,  
C;Superfamily: osteopontin  
C;Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-317/Product: osteopontin #status predicted <MAT>  
F;86-96/Region: aspartic acid-rich  
F;144-146/Region: cell attachment (R-G-D) motif  
F;79/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.3%; Score 111; DB 1; Length 317;  
Best Local Similarity 64.5%; Pred. No. 0.00087;  
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 7 EVFTPVPTVDYDGRGDSVYGRSKSKKF 37  
: |||:|||||:|||||:|||||:|  
Db 129 DVLTPAIPTVDVDPGRGDSLAYGLRSKRSF 159

RESULT 9  
S11449  
collagen short chain - freshwater sponge (Ephydatia muelleri) (fragment)  
C;Species: Ephydatia muelleri  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S11449  
R;Exposito, J.Y.; Quazana, R.; Garrone, R.  
Eur. J. Biochem. 190, 401-406, 1990  
A;Title: Cloning and sequencing of a Porifera partial cDNA coding for a short-chain coll  
A;Reference number: S11449; MUID:90306040; PMID:2163843  
A;Accession: S11449  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-366 <EXP>  
A;Cross-references: UNIPROT:P18503; EMBL:X52598; NID:g9297; PIDN:CAA36831.1; PID:g9298

Query Match 32.3%; Score 107.5; DB 2; Length 366;  
Best Local Similarity 46.6%; Pred. No. 0.0022;  
Matches 27; Conservative 2; Mismatches 10; Indels 19; Gaps 3;

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QY      .      53  PAGPAGPAG  61
        |||||
Db      294  PAGPQPGK  302

RESULT  13
C90769

```

A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: C90769  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-439 <HAY>  
A;Cross-references: UNIPROT:QBXEG4; GB:BA000007; PIDN:BA034546.1; PID:gl3360583; GSPDB: A;Experimental source: strain O157:H7, substrain RMD 0509952  
C;Genetics:  
A;Gene: ECsll123  
C;Superfamily: phage lambda hypothetical protein 401

```

Query Match      29.1%;      Score 97;  DB 2;  Length 439;
Best Local Similarity 44.9%;      Pred No 0.028;
Matches 31; Conservative 5; Mismatches 25; Indels 8; Gaps 4;

QY      1  RRRATEVTTPVPTVDTYDG-RGDSVVYGRS-KSKFRR-----PAGAAG--GPAGPAG 52
db      236  QSRIAAEAVNRITPTVVGGPKGPGPAGPQPKGKGDGTGPAGTGERGPAGDAG 295

```

QY 53 PAGPAGPAG 61  
 |||||  
 Db 296 PAGPQPGKG 304  
  
 RESULT 14  
 S59856  
 collagen alpha 1(iii) chain precursor - mouse

C;date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: S59856; S62120; S16373  
R;Toman, P.D.; de Crombrughe, B.  
Gene 147, 161-168, 1994  
A;Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA  
A;Reference number: S59856; MUID:95011609; PMID:7926795  
A;Accession: S59856  
A;Molecule type: DNA  
A;Residues: 1-1464 <TOM>  
A;Cross-references: UNIPROT:P08121; EMBL:X52046  
R;Toman, D.  
submitted to the EMBL Data Library, November 1994  
A;Reference number: S62120  
A;Accession: S62120





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 27, 2005, 17:57:07 ; Search time 169 seconds  
(without alignments)

190.893 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RSRRAFEVFTVPVPTVDTYD.....AGGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	54.4	314	1	OSTP_HUMAN
2	128.5	38.6	105	2	Q9TSY3
3	128.5	38.6	303	1	OSTP_PIG
4	121.5	36.5	311	1	OSTP_RABIT
5	121	36.3	278	1	OSTP_SHEEP
6	118	35.4	213	2	Q91VH4
7	118	35.4	278	1	OSTP_BOVIN
8	118	35.4	279	2	Q641Z5
9	118	35.4	295	2	Q6PKF3
10	114	34.2	407	2	Q8X5F6
11	113	33.9	294	1	OSTP_MOUSE
12	111	33.3	165	2	Q6N617
13	111	33.3	317	1	OSTP_RAT
14	111	33.3	317	2	P97827
15	108	32.4	200	2	Q6X1Z9
16	108	32.4	358	2	Q9J3U4
17	107.5	32.3	366	1	CAS4_EPHMU
18	107.5	32.3	422	2	Q24893
19	104	31.2	180	2	Q7QNL4
20	104	31.2	191	2	Q7PNG8
21	99.5	29.9	1445	2	Q93251
22	99	29.7	1321	2	Q72202
23	98	29.4	306	2	Q9ACN2
24	98	29.4	1039	2	O50516
25	97.5	29.3	1355	1	CA21_RANCA
26	97	29.1	437	2	Q8X5D0
27	97	29.1	439	2	Q7AFX3
28	97	29.1	604	2	Q91252
29	96	28.8	479	2	Q91A62
30	96	28.8	998	2	Q8CFM4
31	96	28.8	1222	2	Q8K173

32	96	28.8	1464	1	CA13_MOUSE
33	96	28.8	1464	2	Q7TT32
34	96	28.8	1464	2	Q8BKV2
35	96	28.8	1464	2	Q8BLW4
36	95.5	28.7	1464	1	CA11_HUMAN
37	95.5	28.7	1486	2	Q91717
38	95.5	28.7	1486	2	Q7ZTI6
39	95	28.5	283	2	Q44989
40	95	28.5	294	2	Q17459
41	94.5	28.4	809	2	Q93485
42	94.5	28.4	1346	2	Q801M5
43	94.5	28.4	1449	2	Q910C0
44	94	28.2	361	2	Q7AE98
45	94	28.2	437	2	Q9EVE8

P08121	mus musculus
Q7tt32	mus musculus
Q8bkv2	mus musculus
Q8blw4	mus musculus
P02452	homo sapien
Q91717	xenopus lae
Q7zt16	xenopus lae
O44989	caenorhabdi
O74989	caenorhabdi
O17459	caenorhabdi
Q93485	oncorhynch
Q801m5	xenopus lae
Q910c0	oncorhynch
Q7ae98	escherichia
Q9eve8	escherichia

#### ALIGNMENTS

##### RESULT 1

OSTP\_HUMAN STANDARD; PRT; 314 AA.  
AC F10451; Q15681; Q15682; Q15683; Q8NBK2; Q961Z1;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein  
DE 1) (SPP-1) (Urinary stone protein) (Nephropontin) (Uropontin).  
GN Name=SPP1; Synonyms=OPN;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=89263749; PubMed=2726470;  
RA Kiefer M.C., Bauer D.M., Barr P.J.;  
RT "The cDNA and derived amino acid sequence for human osteopontin.";  
RL Nucleic Acids Res. 17:3306-3306(1989).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RX MEDLINE=90353945; PubMed=1974876;  
RA Young M.F., Kerr J.M., Termine J.D., Wewer U.M., Wang M.G.,  
RA McBride O.W., Fisher L.W.;  
RT "cDNA cloning, mRNA distribution and heterogeneity, chromosomal  
RT location, and RFLP analysis of human osteopontin (OPN).";  
RL Genomics 7:491-502(1990).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=92108068; PubMed=1729712;  
RA Shiraga H., Min W., Vandusen W.J., Clayman M.D., Miner D.,  
RA Terrell C.H., Sherbotie J.R., Foreman J.W., Przysiecki C.,  
RA Neilson E.G., Hoyer J.R.;  
RT "Inhibition of calcium oxalate crystal growth in vitro by uropontin:  
RT another member of the aspartic acid-rich protein superfamily.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:426-430(1992).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=95394452; PubMed=7665163;  
RA Crosby A.H., Edwards S.J., Murray J.C., Dixon M.J.;  
RT "Genomic organization of the human osteopontin gene: exclusion of the  
RT locus from a causative role in the pathogenesis of dentinogenesis  
RT imperfecta type II.";  
RL Genomics 27:155-160(1995).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=95031968; PubMed=7945249;  
RA Hijiya N., Setoguchi M., Matsuura K., Higuchi Y., Akizuki S.,  
RA Yamamoto S.;  
RT "Cloning and characterization of the human osteopontin gene and its  
RT promoter.";  
RL Biochem. J. 303:255-262(1994).

[6] SEQUENCE FROM N.A. (ISOFORMS A; B AND C).  
RX MEDLINE=95139605; PubMed=7837791;  
RA Saichou Y., Kuratsu J., Takeshima H., Yamamoto S., Ushio Y.;  
RT "Expression of osteopontin in human glioma. Its correlation with the  
RT malignancy.";  
RL Lab. Invest. 72:55-63(1995).  
[7] SEQUENCE FROM N.A. (ISOFORM B).  
RP TISSUE=Brain;  
RC Yu W., Sarginson J., Gibbs R.A.;  
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
[8] SEQUENCE FROM N.A. (ISOFORM D).  
RP TISSUE=Placenta;  
RC PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togai S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Kotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shionata N., Sano S.,  
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Negase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
[9] SEQUENCE FROM N.A. (ISOFORMS A AND B).  
RP TISSUE=Brain, and Kidney;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg R., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywiniski M.I., Skalska U., Smalilus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[10] SEQUENCE OF 67-278 FROM N.A.  
RP TISSUE=Kidney;  
RX MEDLINE=92246977; PubMed=1575754;  
RA Kohri K., Suzuki Y., Yoshida K., Yamamoto K., Amasaki N., Yamate T.,  
RA Umekawa T., Iguchi M., Sinochira H., Kurita T.;  
RT "Molecular cloning and sequencing of cDNA encoding urinary stone  
RT protein, which is identical to osteopontin.";  
RL Biochem. Biophys. Res. Commun. 184:859-864(1992).  
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an  
CC integral part of the mineralized matrix. Probably important to  
CC cell-matrix interaction.  
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of  
CC interferon-gamma and interleukin-12 and reducing production of  
CC interleukin-10 and is essential in the pathway that leads to type  
CC I immunity (By similarity).  
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=A; Synonyms=OPN-a, OP1B;  
CC IsoId=PI0451-1; Sequence=Displayed;  
CC Name=B; Synonyms=OPN-b, OP1A;  
CC IsoId=PI0451-2; Sequence=VSP\_003778;  
CC Name=C; Synonyms=OPN-c;  
CC IsoId=PI0451-3; Sequence=VSP\_003777;  
CC Name=D;  
CC IsoId=PI0451-4; Sequence=VSP\_011639;  
CC -!- PTM: Extensively phosphorylated on serine residues.  
CC -!- PTM: N- and O-glycosylated.  
CC -!- DISEASE: This protein plays a principal role in urinary stone  
CC formation as the stone matrix.  
CC -!- SIMILARITY: Belongs to the osteopontin family.  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: X13694; AAA31984.1; -;  
CC EMBL: J04765; AAA59974.1; -;  
CC EMBL: M83248; AAA17675.1; -;  
CC EMBL: U20758; AAA86886.1; -;  
CC EMBL: D14813; BAA03554.1; -;  
CC EMBL: D28759; BAA05949.1; -;  
CC EMBL: D28760; BAA05950.1; -;  
CC EMBL: D28761; BAA05951.1; -;  
CC EMBL: AF052124; AAC28619.1; -;  
CC EMBL: AK075463; BAC11635.1; -;  
CC EMBL: BC007016; AAH07016.1; -;  
CC EMBL: BC017387; AAH17387.1; -;  
CC EMBL: BC022844; AAH22844.1; -;  
CC PIR: S50038; S09575  
CC GlycoSuiteDB; P10451; -;  
CC GenSeq; HGNC:11255; SPPI.  
CC H-InvDB; HIX0004361; -;  
CC MIM; 166490; -;  
CC GO: GO:0005578; C:extracellular matrix; TAS.  
CC GO: GO:0005125; F:cytokine activity; ISS.  
CC GO: GO:0008083; F:growth factor activity; TAS.  
CC GO: GO:0005178; F:integrin binding; NAS.  
CC GO: GO:0006910; F:anti-apoptosis; ISS.  
CC GO: GO:0007267; P:cell-cell signaling; TAS.  
CC GO: GO:0007160; P:cell-matrix adhesion; NAS.  
CC GO: GO:0030595; P:immune cell chemotaxis; TAS.  
CC GO: GO:0005093; P:induction of positive chemotaxis; TAS.  
CC GO: GO:0030503; P:negative regulation of bone mineralization; NAS.  
CC GO: GO:001503; P:osification; TAS.  
CC GO: GO:0042102; P:positive regulation of T-cell proliferation; TAS.  
CC GO: GO:0045637; P:regulation of myeloid blood cell differenti. . ; TAS.  
CC GO: GO:0042088; P:T-helper 1 type immune response; TAS.  
CC InterPro; IPR002038; Osteopontin.

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DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.

Query Match          54.4%; Score 181; DB 1; Length 314;
Best Local Similarity 97.2%; Pred. No. 4e-10;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ATEVFTVPVPTVDTYDGRGDSVVYGRSKSKKFRP 40
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Db 142 ATEVFTVPVPTVDTYDGRGDSVVYGLRSKSKKFRP 177

RESULT 2
Q9TSY3 ID Q9TSY3 PRELIMINARY; PRT; 105 AA.
AC Q9TSY3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Osteopontin (Fragment).
GN Name=SPPI;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20078367; PubMed=10612243;
RA Knoll A., Stratil A., Cepica S., Dvorak J.;
RT "Length polymorphism in an intron of the porcine osteopontin (SPPI)
RT gene is caused by the presence or absence of a SINE (PRE-1) element.";
RL Anim. Genet. 30:466-466(1999).
DR EMBL; AJ237667; CAB61259.1; -.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0001503; P:ossification; IEA.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
FT NON_TER 1
FT TER 1
FT NON_TER 105
FT TER 105
SQ SEQUENCE 105 AA; 1489 MW; F2FDCBAE560773CB CRC64;

Query Match          38.6%; Score 128.5; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 2.3e-05;
Matches 28; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 5 ATEVFTVPVPTVDTYDGRGDSVVYGRSKSKKFRP 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 ATDV-TPAVPTGDPNDGRGDSVVYGLRSKSKKFRP 42

RESULT 3
IDP_PIG IDP_PIG STANDARD; PRT; 303 AA.
AC P14287;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SPPI-1).
GN Name=SPPI; Synonyms=OPN;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Bone;
RC MEDLINE=90098793; PubMed=2602123;
RX Wrana J.L., Zhang Q., Sodek J.;
RA "Full length cDNA sequence of porcine secreted phosphoprotein-I (SPPI,
RA osteopontin).";
RL Nucleic Acids Res. 17:10119-10119(1989).

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RN SEQUENCE OF 1-18 FROM N.A.
RP MEDLINE=92339454; PubMed=1633816;
RX Zhang Q., Wrana J.L., Sodek J.;
RA "Characterization of the promoter region of the porcine opn
RT (osteopontin, secreted phosphoprotein 1) gene. Identification of
RT positive and negative regulatory elements and a 'silent' second
RT promoter.";
RL Eur. J. Biochem. 207:649-659(1992).
RN [3]
SEQUENCE OF 17-36 AND 172-211.
RP TISSUE=Bone;
RX MEDLINE=90237064; PubMed=2332443;
RA Zhang Q., Domenicucci C., Goldberg H.A., Wrana J.L., Sodek J.;
RT "Characterization of fetal porcine bone sialoproteins, secreted
RT phosphoprotein I (SPPI, osteopontin), bone sialoprotein, and a 23-kDa
RT glycoprotein. Demonstration that the 23-kDa glycoprotein is derived
RT from the carboxyl terminus of SPPI.";
RL J. Biol. Chem. 265:7583-7589(1990).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
CC integral part of the mineralized matrix. Probably important to
CC cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
CC interferon-gamma and interleukin-12 and reducing production of
CC interleukin-10 and is essential in the pathway that leads to type
CC I immunity (By similarity).
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Extensively phosphorylated on serine residues.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Belongs to the osteopontin family.
CC -----
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CC -----
DR EMBL; X16575; CAA34594.1; -.
DR EMBL; M84121; AAA31094.1; -.
DR PIR; S14903; GEPGO.
DR GO; GO:0005578; C:extracellular matrix; ISS.
DR GO; GO:0005125; F:cytokine activity; ISS.
DR GO; GO:0008083; F:growth factor activity; ISS.
DR GO; GO:0005178; F:integrin binding; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0007160; P:cell-matrix adhesion; ISS.
DR GO; GO:0030595; P:immune cell chemotaxis; ISS.
DR GO; GO:0050930; P:induction of positive chemotaxis; ISS.
DR GO; GO:0030502; P:negative regulation of bone mineralization; ISS.
DR GO; GO:0042102; P:positive regulation of T-cell proliferation; ISS.
DR GO; GO:0045637; P:regulation of myeloid blood cell differenti...; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPONTIN; 1.
KW Bion mineralization; Cell adhesion; Cytokine; Direct protein sequencing;
KW Glycoprotein; Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 303 Osteopontin.
FT SITE 154 156 Cell attachment site.
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 303 AA; 33668 MW; 87D6240E24013EF7 CRC64;

Query Match          38.6%; Score 128.5; DB 1; Length 303;
Best Local Similarity 80.0%; Pred. No. 6.5e-05;
Matches 28; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

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QY 5 ATEVTPVPTVDTYDGRGDSVVYGRSKKFFR 39
Db 138 ATDV-TPAVPTGDPNDGRGDSVVYGLRSKKFFR 171

RESULT 4
OSTP_RABIT
ID OSTP_RABIT STANDARD; PRT; 311 AA.
AC F31097; P46631;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SP-P-1) (OC-1).
OS Name=SPPI;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Osteoclast;
RX MEDLINE=92360044; PubMed=1379809;
RA Tezuka K.-I., Sato T., Kamioka H., Nijweide P.J., Tanaka K.,
RA Matsuo T., Ohta M., Kurihara N., Hakeda Y., Kamegawa M.;
RT "Identification of osteopontin in isolated rabbit osteoclasts.";
RL Biochem. J. 307:257-265(1995).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
CC integral part of the mineralized matrix. Probably important to
CC cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
CC interferon-gamma and interleukin-12 and reducing production of
CC interleukin-10 and is essential in the pathway that leads to type
CC I immunity (By similarity).
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Extensively phosphorylated on serine residues.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Belongs to the osteopontin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D11411; BAA01993.1; -
CC EMBL; D16544; BAA03980.1; -
CC PIR; JC1191; JC1191.
CC InterPro; IPR002038; Osteopontin.
CC Pfam; PF00865; Osteopontin; 1.
CC PRINTS; PR00216; OSTEOPTIN.
CC SMART; SM00017; OSTEO; 1.
CC PROSITE; PS00884; OSTEOPTIN; 1.
KW Biomineralization; Cell adhesion; Cytokine; Glycoprotein;
KW Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16 By similarity.
FT CHAIN 17 311 Osteopontin.
FT SITE 155 157 Cell attachment site.
FT CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).
FT CONFLICT 85 85 M -> V (in Ref. 2).
FT CONFLICT 100 100 R -> Q (in Ref. 2).
FT CONFLICT 128 128 E -> ESDE (in Ref. 2).

FT CONFLICT 151 151 T -> I (in Ref. 2).
SQ SEQUENCE 311 AA; 35172 MW; 692750f63b7cb5a5 CRC64;

Query Match 36.5%; Score 121.5; DB 1; Length 311;
Best Local Similarity 76.5%; Pred. No. 0.00033;
Matches 26; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 5 ATEVTPVPTVDTYDGRGDSVVYGRSKKFF 37
Db 138 ATTVEVPTVETVYDGRGDSVAVRLKRSKMF 171

RESULT 5
OSTP_SHEEP
ID OSTP_SHEEP STANDARD; PRT; 278 AA.
AC Q9XSY9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SP-P-1).
OS Name=SPPI; Synonyms=OPN;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RX MEDLINE=99423513; PubMed=10491620;
RA Johnson G.A., Spencer T.E., Burghardt R.C., Bazer F.W.;
RT "Ovine osteopontin: I. Cloning and expression of messenger ribonucleic
RT acid in the uterus during the periimplantation period.";
RL Biol. Reprod. 61:884-891(1999).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
CC integral part of the mineralized matrix. Probably important to
CC cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
CC interferon-gamma and interleukin-12 and reducing production of
CC interleukin-10 and is essential in the pathway that leads to type
CC I immunity (By similarity).
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Extensively phosphorylated on serine residues (By
CC similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the osteopontin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF152416; AAD38388.1; -
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005125; F:cytokine activity; ISS.
CC InterPro; IPR002038; Osteopontin.
CC Pfam; PF00865; Osteopontin; 1.
CC PRINTS; PR00216; OSTEOPTIN.
CC SMART; SM00017; OSTEO; 1.
CC PROSITE; PS00884; OSTEOPTIN; 1.
KW Biomineralization; Cell adhesion; Cytokine; Glycoprotein;
KW Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16 By similarity.
FT CHAIN 17 278 Osteopontin.
FT SITE 152 154 Cell attachment site.
FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 278 AA; 31052 MW; 37D49E1DD1FBFD47 CRC64;

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Query Match      36.3%; Score 121; DB 1; Length 278;
Best Local Similarity 75.0%; Pred. No. 0.00033;
Matches 24; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 8 VFTFPVPTVDTYDGRGDSVVYGRSKSKKPR 39
Db 138 VFTFPPTSTNDGRGDSVAYGLSKSKKPR 169

RESULT 6
Q91VH4 PRELIMINARY; PRT; 213 AA.
AC Q91VH4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Names=Pogz;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC014284; AF14284.1; -.
DR MGD; MGI:2442117; Pogz.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0001503; P:ossification; IEA.
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 213 AA; 23625 MW; 50CCESDDE9E1797 CRC64;

Query Match      35.4%; Score 118; DB 2; Length 213;
Best Local Similarity 65.6%; Pred. No. 0.00051;
Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 7 EVFTFPVPTVDTYDGRGDSVVYGRSKSKKPR 38
Db 48 DTFTFPVPTVDTYDGRGDSVAYGLSKSKRSFQ 79

RESULT 7
OSTP_BOVIN
ID OSTP_BOVIN STANDARD; PRT; 278 AA.

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AC P31096; Q8SPS6;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SPP-1).
GN Name=SPP1; Synonyms=OPN;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=92084141; PubMed=1721033; DOI=10.1016/0378-1119(91)90439-I;
RA Kerr J.M., Fisher L.W., Termino J.D., Young M.F.;
RT "The cDNA cloning and RNA distribution of bovine osteopontin.";
RL Gene 108:237-243(1991).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Korean; TISSUE=Kidney;
RA Lee T.Y., Ju S.K., Nam M.S.;
RT "Cloning of osteopontin (OPN) in Korean native cattle.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE OF 17-22; 44-54; 168-182 AND 221-243.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from the
RT protease peptone fraction of bovine milk.";
RL J. Dairy Res. 60:189-197(1993).
RN [4]
SEQUENCE OF 17-28, AND PHOSPHORYLATION.
RX PubMed=8663267;
RA Salih E., Zhou H.-Y., Glimcher M.J.;
RT "Phosphorylation of purified bovine bone sialoprotein and osteopontin
RT by protein kinases.";
RL J. Biol. Chem. 271:16897-16905(1996).
RN [5]
POST-TRANSLATIONAL MODIFICATIONS.
RC TISSUE=Milk;
RX MEDLINE=96117654; PubMed=8535240;
RA Soerensen E.S., Hoeirup P., Petersen T.E.;
RT "Posttranslational modifications of bovine osteopontin: identification
RT of twenty-eight phosphorylation and three O-glycosylation sites.";
RL Protein Sci. 4:2040-2049(1995).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
CC integral part of the mineralized matrix. Probably important to
CC cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
CC interferon-gamma and interleukin-12 and reducing production of
CC interleukin-10 and is essential in the pathway that leads to type
CC I immunity (By similarity).
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Bone, inner ear, kidney, uterus, lung, brain,
CC epidermis.
CC -!- SIMILARITY: Belongs to the osteopontin family.
CC
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; M6236; AAA30462.1; -.
CC EMBL; AF492887; AAL99081.1; -.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005125; F:cytokine activity; ISS.
CC InterPro; IPR002038; Osteopontin.

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DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPTNTIN; 1.
DR Biomineralization; Cell adhesion; Cytokine; Direct protein sequencing;
KW Glycoprotein; Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16
FT CHAIN 17 278 Osteopontin.
FT SITE 152 154 Cell attachment site.
FT MOD_RES 23 23 Phosphoserine.
FT MOD_RES 24 24 Phosphoserine.
FT MOD_RES 26 26 Phosphoserine.
FT MOD_RES 27 27 Phosphoserine.
FT MOD_RES 60 60 Phosphoserine.
FT MOD_RES 62 62 Phosphoserine.
FT MOD_RES 63 63 Phosphoserine.
FT MOD_RES 76 76 Phosphoserine.
FT MOD_RES 78 78 Phosphoserine.
FT MOD_RES 81 81 Phosphoserine.
FT MOD_RES 95 95 Phosphoserine.
FT MOD_RES 100 100 Phosphoserine.
FT MOD_RES 103 103 Phosphoserine.
FT MOD_RES 115 115 Phosphoserine.
FT MOD_RES 121 121 Phosphoserine.
FT MOD_RES 124 124 Phosphoserine.
FT MOD_RES 178 178 Phosphothreonine.
FT MOD_RES 184 184 Phosphoserine.
FT MOD_RES 188 188 Phosphoserine.
FT MOD_RES 205 205 Phosphoserine.
FT MOD_RES 210 210 Phosphoserine.
FT MOD_RES 233 233 Phosphoserine.
FT MOD_RES 240 240 Phosphoserine.
FT MOD_RES 245 245 Phosphoserine.
FT MOD_RES 256 256 Phosphoserine.
FT MOD_RES 267 267 Phosphoserine.
FT MOD_RES 272 272 Phosphoserine.
FT MOD_RES 274 274 Phosphoserine.
FT CARBOHYD 131 131 O-linked.
FT CARBOHYD 140 140 O-linked.
FT CARBOHYD 145 145 O-linked.
FT CONFLICT 27 27 S -> K (in Ref. 4).
FT CONFLICT 42 42 I -> T (in Ref. 2).
FT CONFLICT 56 56 T -> A (in Ref. 2).
SQ SEQUENCE 278 AA; 30946 MW; EAB6EA39A6D8E6F CRC64;

Query Match 35.4%; Score 118; DB 1; Length 278;
Best Local Similarity 68.8%; Pred. No. 0.00066;
Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 8 VFTPVPTVDTYDGRGDSVYGRSKSKFRR 39
DB 138 VFTPTFTESANDGRGDSVAYGLKRSKFFR 169

RESULT 8
OY Q64125 PRELIMINARY; PRT; 279 AA.
ID Q64125;
AC Q64125;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Early T-lymphocyte activator-1 (Fragment).
GN Name=Sppl; Synonyms=Eta-1/Op;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95272553; PubMed=7753053; DOI=10.1016/0161-5890(95)00053-H;
RA Ono M., Yamamoto T., Nose M.;
RT "Allelic difference in the nucleotide sequence of the Eta-1/Op gene transcript.";
```

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RL Mol. Immunol. 32:447-448(1995).
DR EMBL; S78177; AAB34351.2; -.
DR MGD; MGI:98389; Sppl.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0001503; P:ossification; IEA.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPTNTIN; 1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30939 MW; BOEF5855D0AC14A2 CRC64;

Query Match 35.4%; Score 118; DB 2; Length 279;
Best Local Similarity 65.6%; Pred. No. 0.00067;
Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 7 EVFTPVPTVDTYDGRGDSVYGRSKSKFRR 38
DB 114 DTFTFIVTVDVPGRGDSLAYGLRSKRSFQ 145

RESULT 9
OY Q6PKE3 PRELIMINARY; PRT; 295 AA.
ID Q6PKE3;
AC Q6PKE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC002113; AA02113.1; -.
DR EMBL; BC080720; AA080720.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
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DR PRINTS; PR00216; OSTEOPOINTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPOINTIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 295 AA; 32652 MW; B06998BF87CF9A68 CRC64;
Query Match 35.4%; Score 118; DB 2; Length 295;
Best Local Similarity 65.6%; Pred. No. 0.0007;
Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 7 EVTPVPTVTDYDGRGDSVVYGRSKSKKFR 38
Db 130 DTFTPIPTVTDVDPDGRGDSLAYGLRSKRSFQ 161
RESULT 10
Q8X5F6 PRELIMINARY; PRT; 407 AA.
AC Q8X5F6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative tail fiber protein.
GN OrderedLocuNames=ECS2231;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AP002557; BAB35654.1; -.
DR F01; G90907; G90907.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF06820; Phage fiber C; 1.
SQ SEQUENCE 407 AA; 41291 MW; D2F6C586ABEC3EB CRC64;
Query Match 34.2%; Score 114; DB 2; Length 407;
Best Local Similarity 48.6%; Pred. No. 0.0024;
Matches 34; Conservative 5; Mismatches 23; Indels 8; Gaps 4;
QY 1 RRRATEVTPVPTVTDYDGRGDSVVYGRSKSKKFR----PAGAAG--GPAGPAG 52
Db 234 QSRIAEEAVNRITPVVPGPKGPGAGQPKGDKGERGDTGPAGATGERGPAGDAG 293
QY 53 PAGPAGPAGP 62
Db 294 PAGPAGPAGP 303
RESULT 11
OSTP MOUSE
ID _OSTP MOUSE STANDARD; PRT; 294 AA.
AC P10923; P19008;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SPP-1) (Minopontin) (Early T lymphocyte activation 1 protein)
DE (2AR) (Calcium oxalate crystal growth inhibitor protein).
GN Name=Sppi; Synonyms=Bta-1, Op, Spp-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

RA Cantor H.;  
RT "Eta-1 (osteopontin): an early component of type-1 (cell-mediated)  
RL Science 287:860-864 (2000).  
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an  
CC integral part of the mineralized matrix. Probably important to  
CC cell-matrix interaction.  
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of  
CC interferon-gamma and interleukin-12 and reducing production of  
CC interleukin-10 and is essential in the pathway that leads to type  
CC I immunity.  
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: Extensively phosphorylated on serine residues.  
CC -!- PTM: N- and O-glycosylated.  
CC -!- SIMILARITY: Belongs to the osteopontin family.  
CC -----  
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CC -----  
DR EMBL; X51834; CAA36132.1; -;  
DR EMBL; X13986; CAA32165.1; -;  
DR EMBL; J04806; AAA57265.1; -;  
DR EMBL; X16151; CAA34276.1; -;  
DR EMBL; BC057858; AAH57858.1; -;  
DR PIR; A37818; A37818.  
DR MGD; MGI:98389; Spp1.  
DR GO; GO:0005578; C:extracellular matrix; ISS.  
DR GO; GO:0005125; F:cytokine activity; NAS.  
DR GO; GO:0008083; F:growth factor activity; ISS.  
DR GO; GO:0005178; F:integrin binding; ISS.  
DR GO; GO:0006916; P:anti-apoptosis; NAS.  
DR GO; GO:0007160; P:cell-matrix adhesion; ISS.  
DR GO; GO:0030595; P:immune cell chemotaxis; ISS.  
DR GO; GO:0050930; P:induction of positive chemotaxis; ISS.  
DR GO; GO:0030502; P:negative regulation of bone mineralization; ISS.  
DR GO; GO:0042102; P:negative regulation of T-cell proliferation; ISS.  
DR GO; GO:0045637; P:regulation of myeloid blood cell differenti. . .; ISS.  
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.  
DR InterPro; IPR002038; Osteopontin.  
DR Pfam; PF00865; Osteopontin; 1.  
DR PRINTS; PR00216; OSTEOPONTIN.  
DR PROSITE; PS00884; OSTEOPONTIN; 1.  
KW Biomineralization; Cell adhesion; Cytokine; Direct protein sequencing;  
KW Glycoprotein; Phosphorylation; Sialic acid; Signal.  
FT SIGNAL 1 16 Potential.  
FT CHAIN 17 294 Osteopontin.  
FT SITE 144 146 Cell attachment site.  
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 43 43 L -> P (in Ref. 4).  
FT CONFLICT 99 99 E -> G (in Ref. 3).  
FT CONFLICT 122 122 V -> F (in Ref. 2).  
SQ SEQUENCE 294 AA; 32459 MW; 9D5F32D67ABC53EA CRC64;

Query Match 33.9%; Score 113; DB 1; Length 294;  
Best Local Similarity 62.5%; Pred. No. 0.0022;  
Matches 20; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 7 EVFTPVVTVTDYDGRGDSVYGRKSKKFR 38  
: |||:||||| :||||| :||||| :  
Db 129 DTFPTPIPTVDVNGRGSLSAYGLRSKRSFQ 160

RESULT 12  
Q6N617 PRELIMINARY; PRT; 165 AA.  
AC Q6N617;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Collagen triple helix repeat precursor.  
GN OrderedLocusNames=RPA2801;  
OS Rhodopseudomonas palustris.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Rhodopseudomonas.  
OX NCBI\_TaxID=1076;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CGA009 / ATCC BAA-98;  
RX PubMed=14704707; DOI=10.1038/nbt923;  
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,  
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,  
RA Gibson J.L., Hanson T.E., Bobat C., Torres y Torres J.L., Peres C.,  
RA Harrison F.H., Gibson J., Harwood C.S.;  
RA "Complete genome sequence of the metabolically versatile  
RT photosynthetic bacterium Rhodopseudomonas palustris";  
RL Nat. Biotechnol. 22:55-61(2004).  
DR EMBL; BX572602; CAE28243.1; -;  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0006817; P:phosphate transport; IEA.  
DR InterPro; IPR008160; Collagen.  
DR Pfam; PF01391; Collagen; 1.  
KW Collagen; Complete proteome; Signal.  
FT SIGNAL 1 23 Potential.  
SQ SEQUENCE 165 AA; 15559 MW; 92F507AE948A0F67 CRC64;  
Query Match 33.3%; Score 111; DB 2; Length 165;  
Best Local Similarity 91.7%; Pred. No. 0.002;  
Matches 22; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 41 AGAAG--GPAGPAGPAGPAGPAGP 62  
||||| ||||||| |||||||  
Db 104 AGAAGPAGPAGPAGPAGPAGPAGP 127

RESULT 13  
OSTP RAT  
ID OSTP RAT STANDARD; PRT; 317 AA.  
AC P08721;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein  
DE 1) (SPP-1).  
GN Name=Spp1; Synonyms=2b7, Spp-1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=93054745; PubMed=1429723;  
RA Singh K., Mukherjee A.B., de Vouge M.W., Mukherjee B.B.;  
RA "Differential processing of osteopontin transcripts in rat kidney-and  
RT osteoblast-derived cell lines";  
RL J. Biol. Chem. 267:23847-23851(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87067405; PubMed=3024151;  
RA Oldberg A., Franzen A., Heinegaard D.;  
RA "Cloning and sequence analysis of rat bone sialoprotein (osteopontin)  
RT cDNA reveals an Arg-Gly-Asp cell-binding sequence";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:8819-8823(1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Smooth muscle;  
RX MEDLINE=94013467; PubMed=8408622;  
RA Giachelli C.M., Bae N., Almeida M., Denhardt D.T., Alpers C.E.,  
RA Schwartz S.M.;  
RA "Osteopontin is elevated during neointima formation in rat arteries



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